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CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
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EARLIER FILING DATE: 1998-08-10
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NUMBER OF SEQ ID NOS: 182
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APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
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                                                                  Baton, Dan L.
Ferrara, Napoleone
                Gerritsen, Mary E.
                                Gerber, Hanspeter
                                                                                                                             Botstein, David
                                                                                                                                                     Baker, Kevin P.
Goddard, Audrey
                                                      Fong,Sherman
                                                                                                             Desnoyers, Luc
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CURRENT APPLICATION NUMBER: US/09/96,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/078910
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
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APPLICANT: Ashkenazi, Avi J
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napole
                                                                                     Sequence 319, Application US/09996243 Patent No. 6478825 GENERAL INFORMATION:
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Eaton, Dan L.
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CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted
TITLE OF INVENTION: Acids E:
PERFERENCE: P2730P1C13
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Pred. No. 4.4e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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RESULT 5
US-08-772-440-2
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Best Local :
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APPLICANT: Tang, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO:
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STREET: 9410 Alto
STATE: CA
COUNTRY USA
ZIP: 94304
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
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LENGTH: 284 amino acids
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPULE.

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Vers

CURRENT APPLICATION DATA:

CURRENT APPLICATION UMBER: US/09/055,095
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
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LIBRARY: LUNG.
TOWR: 1355922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                      175
                                                           235 PRSRDCVAILNGMIFSKDCKELKRCVCERRAGMVKPESL
                                                                                     190 KGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQL 228
                                                                                                                                               136 TLLKIDNRNIVEYIKARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED--G
                                                                                                                                                                                  121 VAEKLCR--
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                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                            76 LAKRECQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNA 135
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                                                                                                                  TMLKINKQEDLEFAASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTS
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Sather, Susan
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                 27.8%; Score 350.5; DB 2; 27.6%; Pred. No. 7.4e-30; tive 54; Mismatches 91;
                                                                                                                                                                                                                                                                          -WSVMQRNY
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189 174 Indels Length

Gaps

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Patent No. 6046158
GENERAL INFORMATION:
                                                                                                                                    Patent No.
                                                                                                                                                Sequence 1,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
          GENERAL INFORMATION:
ADLICANT: ADL-YOUNG, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jemnifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
INFORMATION FOR SEQ ID NO: :
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NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
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APPLICANT: Takashima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
CORRESPONDENCE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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o. 6046158
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                                                                                                                                    , Application US/08688342
5871964
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                                                                                                                                                                                                                                       NQSEGPWFWEDGSAFFPNSFQVRNTVPQESLLHNCVWIHGSEVYNQICNTSSYSICEKE
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Takashima, Akira
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ADDRESS
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Pred. No. 3.5e-23;
2; Mismatches 101
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                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                          APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Coli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C.
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/688
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STREET: CA
CTTY: Palo Alto
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STATE: CA
COUNTRY: US
ZIP: 94304
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                                             ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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CLONE: 515847
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TELEPAX: 415-845-4166
                                               CITY:
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5. 5969104
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                                              Palo Alto
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                                                                                                                                                                                                                                                                                                                                                        DGSVISENMEEF---LEDGKGNWNCAYFHNGKWHPTFCENKHYLMCERKAGM 222
                                                                                                                                                                                                                                                                                                                                                                                        MSINSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWE
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Pred. No. 1.7e-22;
84; Mismatches 78;
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                                                                                                                              C-TYPE LECTIN
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COMPUTER READABLE FORM:

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US-08-690-095-1
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                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08690095 Patent No. 5792648
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Best Local Similarity
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
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                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                           APPLICANT: Au Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                OPERATING SYSTEM:
                                             COMPUTER:
                                                                                                            COUNTRY:
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ARE: FastSEQ Version 1.5
APPLICATION DATA:
                                                                                                94304
                                                                                                                                            Palo Alto
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                                                                                                                                                           3: Incyte Pharmaceuticals, 3174 Porter Drive
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RESULT 9
US-09-113-789-1
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Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
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MOLECULE TYPE: p.
IMMEDIATE SOURCE:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
              FILING DATE:
PRIOR APPLICATION DATA:
                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTESEQ VErsion 1.5 CURRENT APPLICATION DATA:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillman, a APPLICANT: Au-Young, APPLICANT: Goli, Sur
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FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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CITY: Palo Alto
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LIBRARY: MLL.
TONE: 513418
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                                               APPLICATION NUMBER:
                                                                                                                                                                                  COUNTRY:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                     3174 Porter Drive
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N: NOVEL HUMAN MACROPHAGE ANTIGEN
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08/690,095
                                               US/09/113,789
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Pred. No. 1.6e-20;
9; Mismatches 102;
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                                            ; TYPE: PRT; ORGANISM: Homo sapiens US-09-482-273-126
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                                                                                      SOFTWARE: Pat
SEQ ID NO 126
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                           Sequence 126, Application US/09482273
Patent No. 6534631
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              Query Match
 Best Local Similarity
                                                                                                                  BARLIER FILING DATE: 1998-07-15
BARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-01-13
                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PZ030P1
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LENGTH: 272 amino acids
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LIBRARY: MELL
TONE: 513418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ELYSKEQEHKCKFCPRRWIWHKDSCYFLSDDVQTWQESKMACAAQNASLLKINNK 174
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28.3%;
20.9%;
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Pred. No. 1.6e-20;
 Score
Pred.
 263.5; DB 4
No. 1.6e-20;
              4.
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              Length 248;
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Best Local :
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RESULT 11
US-08-772-440-13
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Patent No. FORMATION:
                                                                                                                                                                                                                                                                                                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSIT
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
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                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 FFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLI-RWVGLSRQKSNEVWKWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 PAPSHVWRPAALFLTLLCLLLLIGLGVLASMFHVTLKIEMKKMNKLQNISEELQRNISLQ 75
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                                                                                                               1 Similarity 70; Conserv
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QRNYLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFF
                                                                     DEDGYITLNIKT----RKPALVSVGP-ASSFWWRVMALILLLILCVGMVVGLVALGIWSVM
                                        DEDGYTQLDFSTQDIHKRPRGSEKGSRAPSSPWRPIAVGLGILCFVVVVVAAVLG-----
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                                                                                                               Conservative
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                                                                                                                                 20.3%;
                                                                                                                                                                                                                                                                                                                                                                                         32,165
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                                                                                                             Score 255.5; DB 3
Pred. No. 8.8e-20;
16; Mismatches 80
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US-09-055-095-3
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INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF. TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXIDIZED
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LIBRARY: Gell
TOME: 1902984
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OPERATING SYSTEM:
SOFTWARE: FastSE(
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5. 5945308
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                  NCYLFSSGSFNWEKSQEKCLSLDAKLLKINSTADLDFİQQAISYSSFPFWMGLSRRNPSY 213
                                              SCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIK---ARTHLIRWVGLSRQKSNE 168
                                                                                ASQESENELKEMI ETLÄRKLINEKSKE ØMBLHH QNINL QETI KRVANCSAP CPQDWIWHGE
                                                                                                                                               WWCLAAATLGVLCLGLVVTIMVLGMQLSQVSDLLTQEQANLTHQKKKLEGQISARQQAEE 93
                                                                                                                                                                              WWRVMALILLICVGMVVGLVALGIWSVMQRNYLQDENENRT-----
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                                                                                                                                                                                                                                           Length 273;
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Matches
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Patent No. 5962260
GENERAL INFORMATION:
                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NÜMBER: 24408
REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 816-9479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-NOV-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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COUNTRY:
                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                               ASQESENELKEMIETLARKLNEKSKEQMELHHQNENLQETLKRVANCSAPCPQDWIWEGE
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Pred. No. 6.2e-19;
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--CAYFHNGKMHPTFCENKHYLMCERKAG 221
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
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APPLICANT: Masaki, TO
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-7UL-1995
ATTORNEY/AGENT INFORMATION:
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STREET: New York
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REGISTRATION NUMBER:
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                                          NCYLFSSGSFNWEKSQEKCLSLDAKLLKINSTADLDFIQQAISYSSFPFWMGLSRRNPSY
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Pred. No. 6.2e-19;
0; Mismatches 78;
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RESULT 15
US-08-809-494A-4
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Patent No. 5962260
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-NOV-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,49
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ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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SEQUENCE CHARACTERISTICS
LENGTH: 273 amino acids
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APPLICATION NUMBER: JP 7
FILING DATE: 31-JUL-1995
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TOPOLOGY:
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OPERATING SYSTEM:
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STREET: 261 Madison Avenue
CITY: New York
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REGISTRATION NUMBER:
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196 HSSFPFWMGLSMRKPNYSWLWEDGTFLTPHLFR-IQGAVSRMYPSGTCAYIQRGTVFAEN
                                152 RTHLIRWVGLSROKSNEVWKWEDGSVISENWFEFLEDGKGNM----NCAYFHNGKWHPTF
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.8e-18;
5; Mismatches 85;
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US-09-352-302-4
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REFERENCE/DOCKET NUMBER: JG
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COTTRET: 261 Madison Avenue
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REGISTRATION NUMBER: 244
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RTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNM----NCAYFHNGKMHPTF
                                                                                                                                                                                                                                                -----QQLAKRFCQYVVKQS--ELKGTFK--GHK---
                                                                                                                                                                                                                                                                                                                                               KPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTL--
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                                                                                               AANYSGPCPQDWLWHEENCYQFSSGSFNWEKSQENCLSLDAHLLKINSTDELEFIQQMIA 195
                                                                                                                                                                                               QEDILEGQILAQRRSEKSAQESQKELKEMIETLAHKLDEKSKKLMELHRQNLNLQEVLKE 135
                                                                                                                                                                                                                                                                                              KTAKGTTGFVSSWRWYPAAVTLGVLCLGLLVTVILL----ILQLSQVSDLIKKQQANITH 75
                                                                                                                                                ----CSPCDTNWRYYGDSCYGFFRHNLTWEBSXQYCTDMNATLLKIDNRNIVEYIK---A 151
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24.9%;
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Pred. No. 2.8e-18;
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US-09-055-095-4
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICANT: Patterson, Chanc
APPLICANT: Corley, Neil C.
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APPLICATION DATA:
APPLICATION NUMBER: US/09/055.006
FILING DATE: Filed "FOR CLASSIFF TO THE PROPERTY OF THE PROPERTY
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SITY: Palo Alto
CITY: Palo Alto
TWATE: CA
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LIBRARY: GenBar
CLONE: 1902982
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TSLECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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  188 QQMIAHSSFPFWMGLSMRKPNYSWLWEDGTPLTPHLFR-IQGAVSRMYPSGTCAYIQRGT 246
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                                         K---ARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNM----NCAYFHNGK 202
                                                                                                                                                                                               ANITHQEDILEGQILAQRRSEKSAQESQKELKEMIETLAHKLDEKSKKLMELHRQNLNLQ 127
                                                                                               EVIKEAANYSGPCPQDWIMHEENCYQFSSGSFNWEKSQENCLSIDAHLIKINSTDELEFI
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                                                                                                                                                                                                                                                                                              -GFVSSWRWYPAAVTIGVICLGLLVTVILL----ILQLSQVSDLIKKQQ
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Pred. No. 3.5e-18;
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US-08-809-494A-2
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Best Local S
Matches 66
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Patent No. 5962260
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 270 amino acids
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Local Similarity 25.2%; Pred. No. 3.5e-18;
nes 66; Conservative 54; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 6-321705 FILING DATE: 30-NOV-1994
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   MHPTFCENKHYLMCERKAGMTK 224
                                                                  K---ARTHLIRWVGLSRQKSNEVWKWEDGSVISENWFEFLEDGKGNM----NCAYFHNGK 202
                                                                                                                                                                                                                            NGKTAK-----GFVSSWRWYPAAVTLGVLCLGLLVTVILL----ILQLSQVSDLIKKQQ 67
                                                                                                                                                                                                                                                            NIKTRKPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRT 70
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                                   QQMIAHSSFPFWMGLSMRKPNYSWLWEDGTPLTPHLFR-IQGAVSRMYPSGTCAYIQRGT 246
                                                                                                  EVLKEAANYSGPCPODWLWHEENCYOFSSGSFNWEKSQENCLSLDAHLLKINSTDELEFI
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261 Madison Avenue
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                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                              --CSPCDINWRYYGDSCYGFFRHNLIWBESKQYCIDMNAILLKIDNRNIVEYI 149
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US-09-352-302-2
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Matches
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                                                                                                                                                                                                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-NOV-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
FILING DATE: 30-NOV-1994
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TELEPHONE: 212 986-4090
TELEPAX: 212 818-9479
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ATTORNEY/AGENT INFORMATION:
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CTTY: New York
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ZIP: 10016-2391
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128 EVLKEAANYSGPCPODWLWHEENCYOFSSGSFNWEKSOENCLSIDAHLLKINSTDELEFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 NIKTEKPALVSVGPASSFWMRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENET 70
                                                                K---ARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGXGNM----NCAYFHNGK 202
QQMIAHSSFPFWMGLSMRKPNYSWLWEDGTPLTPHLFR-IQGAVSRMYPSGTCAYIQRGT 246
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RESULT 20
US-08-772-440-8
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US-08-772-440-31
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                                                                                          Patent No. 6046158
GENERAL INFORMATION:
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GENERAL INFORMATION:
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                                                                                                                             Sequence
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INFORMATION FOR SEQ ID NO:
APPLICANT: Ariizumi, Kiyoshi
APPLICANT: TAKAShima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
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TITLE OF INVENTION:
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APPLICANT: Takashima,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 32,165
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10. 6046158
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33.5%;
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; Pred. No. 5.2e-18; 
24; Mismatches 74;
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US-08-772-440-10
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Matches
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ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                       TITLE OF INVENTION: TITLE OF INVENTION:
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STRY: Houston
TTY: Toxas
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ZIP: 77210
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STREET: P.O.
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                                                                                                                                          Houston: Texas
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Sequence 10, Application US/08772440 Patent No. 6046158
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                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0,
CURRENT APPLICATION DATA:
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TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 33.5%; Pred. No. 5.3e-18;
hes 56; Conservative 24; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UT
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GNSWYGSKRHCSQLGAHLLKIDNSKEFEFIESQTSSHRINAFWIGLSRNQSEGPWFWEDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAFFPNSFQVRNTVPQESLLHNCVWIHGSEVYNQICNTSSYSICEKE 179
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Takashima, Akira
                                                                                                                                                                                                                                                                                               Arnold,
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US/08/772,440
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                                                   Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                             COMPOSITIONS AND USES
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US-08-543-246B-9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: CONCURSION 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
NAME: Parker, David J.
1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 10:
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LENGTH: 126 amino acid
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                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DN
TITLE OF INVENTION: na
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                    FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                        PRIOR APPLI
TELECOMMUNICATION INFORMATION:
               NAME: Kassenoff, Melvyn M. REGISTRATION NUMBER: 26,389 REFERENCE/DOCKET NUMBER: 111
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                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        FILING DATE: 27-MAR-:
RIOR APPLICATION DATA:
                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 27-MAR-1992
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 07901-1027
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                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 221.5; DB 3 36.0%; Pred. No. 2.2e-16; tive 20; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA and amino acid sequence specific for natural killer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08543246B
                                                                                                         US 08/122,514
                                                                                                                                                            PCT/US92/02469
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                   118-7704/PCT/CONT
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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                            FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: KASSENGTE, MELVYN M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6927
                                                     INFORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
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OTTY: Summit,
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les 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
LENGTH: 216 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 PTNGSWQWEDGSILSPNLLTIIEMQKG--DCALYASSFKGYIENCSTPNTYICMQR 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 KSNEVWKWEDGSVISENWFEFLEDGKGNMNCA-YFHNGKMHPTFCENKHYLMCERK 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA and amino acid sequence specific natural killer cells
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US-08-543-246B-20
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                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/122,514 FILING DATE: 24-SEP-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 27-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                 NAME: Kassenoff, Melvyn M. REGISTRATION NUMBER: 26,38 REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 07901-1027
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                                   TOPOLOGY:
                                                 STRANDEDNESS:
                                                                                                                                                 TELEPHONE:
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                                                                                  ENGTH:
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o. 6262244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
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                                                                amino acid
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                                                                                  134 amino acids
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No. 6262244artis Corporation
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29.0%;
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                                                                                                                                                                                             26,389
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Pred. No. 5.8e-15;
5; Mismatches 57;
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US-08-690-095-9
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                                                           Matches
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                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/6
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                             IMMEDIATE SOURCE
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                                                                                                                     LIBRARY: GGAL
TYONE: 1098617
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                                                                       Local
                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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CITY: Palo Alto
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                                                                                                                                                                                                                                       ENGTH:
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5, 5792648
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                          30 WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRIGILQQLAKRFCQYVVKQSE 89
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                                                                         Similarity
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Goli, Surya K.
VENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
                                                         Conservative
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                                                        Score 195.5; DB 1;
Pred. No. 2.4e-13;
87; Mismatches 79;
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; MOLECULE TYPE:
US-08-650-578-2
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GENERAL INFORMATION:
                                                                                                                                                Matches
                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
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ADDRESSEE: DNAX Rese
                                                                                                                                                                                                                                                                                                                                   NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXX
TELECOMMUNICATION INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                   TYPE:
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                              45 TPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDE 104
                                                         90 LKG----TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNI 145
                                                                                                                   30 WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSE 89
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                                                                                      9 WRLISGTIGITCLSL---MATLGI
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                                                                                                                                                              Similarity
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California
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Lopez-Botet, Miguel
Phillips Jr., Joseph H
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                                                                                                                                                Conservative
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                                                                                                                                              37;
                                                                                                                                           Score 195.5; Db 2;
Pred. No. 2.4e-13;
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US-08-688-342-3
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LIBRARY: GenBar
CLONE: 1098616
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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CTTY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
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APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    / Match 15.5%; Score 195.5; DB 2; Local Similarity 24.6%; Pred. No. 2.4e-13; nes 48: Conservative 37; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 DESCEDKNRYICKQQ 177
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                                           205 PTFCENKHYLMCERK 219
                                                                                                                                                                                                                               90 LKG----TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEBSKQYCTDMNATLLKIDNRNI 145
                                                                                                                                                                                                                                                                                                                      30 WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSE 89
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                                                                                                                                  VEYIKARTHLIRWVGLSROKSNEVWKWEDGSVISENMFEFLEDGKGNMNC-AYFHNGXMH 204
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DESCEDIONRYICKOO 177
                                                                                         LDFMSS-SQQFYWIGLSYSEEHTAWLWENGSALSQYLFPSFET-FNTKNCTAYNPNGNAL 162
                                                                                                                                                                                  TPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDE
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3174 Porter Drive
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Cocks, Benjamin G.
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RESULT 30
US-09-113-789-9
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US-09-113-788-3
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PATENT NO. 5969104
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                           Best
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1098616
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                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                     163 DESCEDKNRYICKQQ 177
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                                                                                                                                                                                                                                                   90 LKG----TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKCYCTDMNATLLKIDNRNI 145
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     Application US/09113789
                                                                                                                     PTFCENKHYLMCERK 219
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                                                                                                                                                                                    VEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNC-AYFHNGKMH 204
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3174 Porter Drive
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IBM Compatible
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24.6%; Pred. No. 2.4
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7; Mismatches 79;
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RESULT 31
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GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line
MOLECULE TYPE: F
IMMEDIATE SOURCE:
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MEDIUM TYPE: Diskette
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ZIP: 943
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CLONE: 1098617
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REGISTRATION NUMBER: 36,749
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                                                            163 DESCEDKNRYICKQQ 177
                                                                                            205 PTFCENKHYLMCERK 219
                                                                                                                                                                                         45 TPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDE
                                                                                                                                                                                                                       90 LKG----TFKGHKCSPCDTNWRYYGDSCYGFFRENLTWEESKQYCTDMNATLLKIDNRNI 145
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48; Conserv
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                                                                                                                            LDFMSS-SQQFYWIGLSYSEEHTAWLWENGSALSQYLFPSFET-FNTKNCTAYNPNGNAL 162
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                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                      15.5%; Score 195.5; DB 3; 24.6%; Pred. No. 2.4e-13; tive 37; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 10, Application US, Patent No. 6277959
GENERAL INFORMATION:
APPLICANT: Valladeau, Je
APPLICANT: Ravel, Odile

US/09111470

APPLICANT:

Bates, Elizabeth E.M.

Jenny

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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
                                                                                                                                                                                                            GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Mammalian Membras
TITLE OF INVENTION: Related Reagents
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CORRESPONDENCE ADDRESS:
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                                                                                             APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
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                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                        STREET:
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ELECTION ADDRESS:

Incyte Pharmaceuticals, Inc.
ET: 3174 Porter Drive
Palo Alto
E: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                   KYCOLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEG--AWKWVDGTDYATG-FQNW 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYCTDMNATLLKIDNRNIVEYI-KARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (650)852-9196
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28.6%;
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Pred. No. 1.2e-12;
2; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4,
                                                                                                                                                                                                                                                                                                                                                  Patent No. 5969104
GENERAL INFORMATION:
APPLICANT: AU-YOUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
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                                                SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA
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OPERATING SYSTEM:
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CLONE: 1235724
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TOPOLOGY: lir
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                                                                                                                                                 ZIP:
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CITY: Palo Alto
                                                                              OPERATING SYSTEM:
                                                                                                                                                     COUNTRY: U
ZIP: 94304
                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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              FILING DATE
                                 APPLICATION NUMBER:
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Goli, Surya K.
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28.6%; Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                          Janice
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                                   US/09/113,788
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US-09-111-470-4
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                 ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Membrar
TITLE OF INVENTION: Related Reagents
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LENGTH: 292 amino acids
FILING DATE: 09-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                   APPLICATION NUMBER: US/0: FILING DATE: 08-JUL-1998
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                                                                     CLASSIFICATION:
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CLONE: 1235724
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                                                                                                                                                                                                                                          COUNTRY:
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48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQDLKKLTCQVATLNNNGEEASTEGT-----C--CPVNWVEHCDSCYWFSHSGMSWAEAE 182
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Bates, Elizabeth E.M
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                                   US 60/053,080
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                                                                                                   US/09/111,470
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Pred. No. 1.3e-12;
2; Mismatches 61;
                                                                                                                                     Version
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Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: ECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
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Best Local
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                  TBLEFAX: (202) 737-352
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
CORRESPONDENCE HROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                        FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION NOMBER: PCT/US95/04258
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION NUMBER: IL 109257
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REFERENCE/DOCKET NUMBER: SF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/722,126A
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                          NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      FILING DATE: 08-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (M
                                              TELEPHONE: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 K-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 VQDLKKLTCQVATLNNNASTEGT-----C--CPVNWVEHQDSCYWFSHSGMSWAEAEKYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 QLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEG--AWKWVDGTDYATG-FQNWKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 TDMNATLLKIDNRNIVEYI-KARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 QPDDWQGHGLGGGEDCAHFHPDGRWNDDVCQRPYHWVCEAGLGQT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 LQQLAKRFCQYVV--KQSELKGTFKGHKCSFCDTNWRYYGDSCYGFFRHNLTWEESKQYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 15.1%; Score 190; DB 3; Similarity 29.1%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 316 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.C.
129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAL, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                          (202) 628-5197
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                                                        737-3528
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                                                                                                                  PECHT=1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAFA)
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PCT-US95-04258-10
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                                                                                                                      PCT-US95-04258-10
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Best Local 9
                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                            TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IL 1
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-APK-1553
PRIOR APPLICATION DATA:
PRIOR TOATION NUMBER: IL 109257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                       Local Similarity
                                                                                                                                                               TYPE: amino a
                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                   NAME: BROWDY, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 CDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEY-IKARTHLIRWVG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 KHYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 LSRQKSNEVWKWEDGSVISENM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                            102 CDINWRYYGDSCYGFFRHNLTWEESKQYCIDMNATLLKIDNRNIVEY-IKARTHLIRWYG
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                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNRWVCEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTDRDGS--WKWVDGTDYRSNYRNWAFTQPDNWQGHEQGGGEDCAEILSDGHWNDNFCQQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.C.
CPVNWVEFGGSCYWFSRDGLTWAEADQYCQLENAHLLVINSREEQDFVVKHRSQFHIWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                          ON NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                          202-737-3528
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                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MASA) 10
                                                                         14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                             PCT/US95/04258
                                                                                                                                                                                                                                                                                                                   25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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Pred. No. 1.1e-12;
2; Mismatches 53;
                                                                                                                                                                                                                                                                                                        PECHT=1
                                                           Score 187.5; DB 5;
Pred. No. 1.1e-12;
2; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FEFLEDGKGNMNCAYFHNGKMHPTFCEN 210
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                                                              Indels
                                                                                       Length 129;
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US-08-722-126A-5
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                                                                                                                               β
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                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-722-126A-5
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                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
PILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 11 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY. Romon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 C.
CITY: Washington
CTATE: D.C.
TMITTED ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL HITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (WAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: ZIP: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 08-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 VNRWVCEKR 127
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94
                                                               53
                                                                                                 61
                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20004
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                  (: 188 amino acids amino acid 
amino acid 
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHYLMCERK 219
                                                                                            YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFREN
                                                                                                                             RDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFY---WIGL-
                            LTWEESKQYCTDMNATLLKI-DNRNI---VEYIKARTHLIRWVGLSRQKSNEVWKWBDG- 175
                                                                 LLLYQRTLCCGS-
                                                                                                                                                                 MQDEDGYITLNIKTRKPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAL, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PECHT, Israel GUTHMANN, Marcelo D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                   13.9%; Score 175.5; DB 3 26.9%; Pred. No. 3.8e-11; ative 32; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/722,126A
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                                                                 -KG-FMCSQCSRCPNLWMRNGSHCYYFSMEK 93
                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #1.30
                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                 Length 188;
                                                                                                                                                                                                    Indels
   -RDIDGWRWEDGP 147
                                                                                                                                                                                                    51;
                                                                                                                                                                                                    Gaps
                                                                                                                                                                    60
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RESULT 39
US-08-690-095-8
; Sequence 8, Applica:
; Patent No. 5792648
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PCT-US95-04258-5
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Best Local Similarity 26.9%; Pred. No. 3.8e-11;
Matches 61; Conservative 32; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PER
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                RDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGBDFY---WIGL---RDIDGWRWEDGP 147
                                                                                                                                                                                                LTWEESKQYCTDMNATLLKI-DNRNI---VEYIKARTHLIRWVGLSRQKSNEVWKWEDG- 175
                                                                                                  ALSISIISNSVVQ----
                                                                                                                                ---SVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCER 218
                                                                                                                                                                                                                                                                 YLQDENENRTGTLQQLAKRFCQYVVXQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN 120
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                 Application US/08690095
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 amino acids
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202-737-3528
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                             Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Solly Surya K.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE
NUMBER OF SEQUENCES: 9
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APPLICANT: Hillman, Jennifer
APPLICANT: Au-Young, Janice
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
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LIBRARY: GenBa
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                   CORRESPONDENCE ADDRESS:
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etreet: 3174
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CITY: Palo Alto
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 Incyte Pharmaceuticals,
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rya K.
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Pred. No. 7.5e-11;
8; Mismatches 86
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COMPUTER READABLE FORM:

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US-08-543-246B-2
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Best Local Similarity
                                                                                                                                                                                          Sequence 2, Application Patent No. 6262244 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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                                                                                                                TITLE OF INVENTION: DN
TITLE OF INVENTION: na
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sin
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COUNTRY: US
CIP: 07901-1027
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                                                                                  ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
                                                     CITY: Summit,
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CA
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                                                                                                                                                                                                                                                                                                                                                                  SSWIGVERNSSHHPWVTMNGLAFKH--
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                                                                      564 Morris Avenue
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                                                                                                  Michael W. Glynn
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23.9%;
                                                                                                                                             DNA and amino acid sequence specific natural killer cells
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RESULT 42
US-08-543-246B-21
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-MAR-1992
PROR APPLICATION DATA:
APPLICATION UNMER: US 08/11
PILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-MAR-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                            APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patenti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/543,246B
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                                                                                                                        ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                         CITY: Summit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 SSWIGVFRNSSHIPWVTMNGLAFKH---EIKDSDNAELNCAVLQVNRLKSAQCGSSIIXH 228
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                                                                                                                                                                                                                                                                                                                                                                                                   229 CKHK 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 ILGIICLILMASVVTI---VVIPSTLIQRHNNSSLNTRTQ
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.8%;
23.9%;
                                                                                                                                                                                                                  {\tt DNA} and amino acid sequence specific for natural killer cells
                                                                                                                                                                                                                                                                                                          US/08543246B
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RESULT 43
US-08-690-095-6
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                                                                                                                                         Sequence 6, Application US/08690095
Patent NO. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: MOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acid
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HYPOTHETICAL: N
ANTI-SENSE: NO
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PRIOR APPLICATION NUMBER: US 07/676,663
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APPLICATION NUMBER: US 0:
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/1
FILING DATE: 27-MAR-1992
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COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                  STATE:
                                                                                                 STREET:
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                                                                                                ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                              172 SSWIGVFRNSSHHPWVTMNGLAFKH---EIKDSDNAELNCAVLQVNRLKSAQCGSSIIYH 228
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                                                                                Palo Alto
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23.9%;
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                                                                                                                 Inc
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US-09-113-789-6
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Best Local
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Sequence 6, Applic Patent No. 6034219
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
PAPPLICATION NUMBER: US/09/113,
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Au-Young, APPLICANT: Goli, Sury
                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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LIBRARY: GenBa
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                                                                                                                                                                                                                       STREET: 31/.
CTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 KHYLMCERK 219
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Similarity 22.8%;
                                                                                                                                                                                       94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09113789
                                                                                                                                                                                                    U.S.
                                                                                                                                                                                                                                                           3174 Porter Drive
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415-845-4166
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                                                                                                                             IBM Compatible
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                                                                                                                                                  Diskette
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                                                                                                              DOS
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ya K.
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   08/690,095
                                                         US/09/113,789
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Pred. No. 4.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application Patent No. 6262244
GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 35061
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
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                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                         ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
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STREET: __
Summit,
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           APPLICATION NUMBER: PCT/1
FILING DATE: 27-MAR-1992
                                                                                                 APPLICATION NUMBER: US/08/543,246B FILING DATE:
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APPLICATION DATA
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No. 6262244artis Corporation
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Pred. No. 4.3e-10;
                                                                                                                                                                                                                                                                                                                                                          amino acid sequence specific for killer cells
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GENERAL INFORMATION:
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201-1027

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                        FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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FILING DATE: 24-SEP-1993
ANTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6927
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE:
STREET: 564
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                                     FILING DATE:
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E: No. 6262244artis
564 Morris Avenue
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                                 UMBER: US 08/122,514
24-SEP-1993
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RESULT 47
US-09-517-605-2
                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-517-605-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US~08-543-246B-23
                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09517605 Patent No. 6391567
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Van Kooyk, Yvette
APPLICANT: Geijtenbeck, Tneo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVERAL ENTRY INTO
TITLE OF INVENTION: CBLLS
FILE REFERENCE: 1049-1-017
CURRENT FALLING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kassenoff, Melvyn REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                          l Similarity
38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                CKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYW 343
                                                CTDMNATLLKI---DNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMIYHCKHK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLTAEVLGIIC----IVLMATVLKTIVLIPFLEQNNSSPNTRTQ---------
                                                                                                                     GTLQQLAKRFCQYVVKQ-SELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCEN 210
                                                                                     GELPEKSKQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KARHCGHCPEEWITYSNSCYYIGKERRTWEBSLLACTSKNSSLLSIDNEEEIKFL- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASILPSSWIGVFRNSSHHPWVTINGLAFKH---KIKDSDNAELNCAVLQVNRLKSAQCGS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                          Conservative
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                                                                                   -QEIYQELTQLXAAVE-RLCHPCPWEWTFFQGNCYFMSNSQRNWHDSITA
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26,389
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Pred. No. 4.3e-10;
12; Mismatches 86
                                                                                                                                                      Score 164.5; DB 4
Pred. No. 1.8e-09;
7; Mismatches 79
                                                                                                                                                                                         DB 4;
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Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGRNT INFORMATION:
NAME: Kassenoff, Melvyn M.
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: F19999 disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kassenoff, Me
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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128
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                                                                                                                                                                                                                             Similarity
IYHCKEK 134
                               YLMCERK 219
                                                                    SP-SSWIGVFRNSSHHPWVTMNGLAFKH---EIKDSDNAELNCAVLQVNRLKSAQCGSSI 127
                                                                                                                                       TQKARHCGHCPEEWITYSNSCYYIGKERRTWEESLLACTSKNSSLLSIDNEEEMKFLSII
                                                                                                                                                                       TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKAR 152
                                                                                                    THLIRWVGLSRQXSNEVWXWEDGSVISENMFEFLEDGXGNMNCAYFHNGXMHPTFCENKH 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                            135 amino acids
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No. 6262244artis
                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                     : protein
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                                                                                                                                                                                                                                                                                                  C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA and amino acid sequence specific natural killer cells
                                                                                                                                                                                                                           13.0%; Score 164; DB 3; 27.6%; Pred. No. 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
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                                                                                                                                                                                                              19;
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RESULT 49
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                                                                                                                                                                                    Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-MAR-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 24-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DALE:
PRIOR APPLICATION DATA:
O7/676,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                             ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kassenoff, Melvyn M. REGISTRATION NUMBER: 26,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
   128 IYHCKHK 134
                              213 YLMCERK 219
                                                                                        153 THLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKH 212
                                                                                                                                                     93
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12
                                                                                                                                                                                   l Similarity
35; Conserv
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                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                             ILPSSWIGVERNSSHHPWVTINGLAFKH---KIKDSDNAELNCAVLQVNRLKSAQCGSSM 127
                                                                                                                                                    TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKAR 152
                                                                                                                       TQKARHCGHCPEEWITYSNSCYYIGKERRTWEESLLACTSKNSSLLSIDNEEEIKFL-AS
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                                                                                                                                                                                                 Score 163; DB 3;
Pred. No. 5.4e-10;
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                    69;
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RESULT 50

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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: No. 6262244artis
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CURRENT APPLICATION NUMBER: US/09/903,190
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/PRIOR APPLICATION NUMBER: 60/
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RESULT 2
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SOFTWARE: Pates
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FRIGHH: 229
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Publication No. US20030162176A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jear
APPLICANT: Duclert, Aymeric
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Best Local :
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLGS
CURRENT APPLICATION NUMBER: U0/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/06787
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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APPLICANT: Ashkenazi,Avi J
APPLICANT: Baker Kevin P.
APPLICANT: Botstein,David
APPLICANT: Desnoyers,Luc
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RESULT 3
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PRIOR APPLICATION NUMBER: 60/887827
PRIOR FILING DATE: 1998-06-03
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PRIOR APPLICATION NUMBER: 60/088025
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PRIOR APPLICATION NUMBER: 60/088026
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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR PRIOR PARTICATION NUMBER: 60/067370
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-04-28
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APPLICATION 1
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Ferrara, Napoleone
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                   NUMBER: 60/088028
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088655
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DR APPLICATION NUMBER: 60/091982

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APPLICATION NUMBER: 60/091633
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730P1C56
FULL REPERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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APPLICANT: Baker, Kevin P
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L
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OF INVENTION: Acids
REFERENCE: P2730P1C65
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Kljavin, Ivar J.
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art, Timothy A.
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S-09-989-731-424
Sequence 424, Application
Patent No. US20020103125A1
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zaang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273010170
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06251
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DR APPLICATION NUMBER: 60/078910
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OR APPLICATION NUMBEE: 60/083322
OR FILING DATE: 1998-04-28
                                                                           DR FILING DATE: 1997-10-17

OR APPLICATION NUMBER: 60/65186

OR FILING DATE: 1997-11-12

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No. US20020123463A1
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Kljavin, Ivar J.
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Godowski, Paul
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APPLICANT: Williams, P. Mickey
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APPLICANT: Wood, William I.
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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
ITITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273021C8
CURRENT APPLICATION NUMBER: US/09/990,442
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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Gurney,Austin L.
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Botstein, David
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, p. Mickey
APPLICANT: Wold, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembre
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
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DR FILING DATE: 1998-06-10
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: Baker, Kevin P
: Botstein, David
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                                                                  Roy,
Stewart, 'i.m.'
Stewart, 'i.m.'
Daniel
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Grimaldi, J. Christopher
Gurney, Austin L.
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Godowski, Paul
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Gerritsen, Mary E.
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Ferrara, Napoleone
                           Watanabe, Colin I
Williams, P. Mich
Wood, William I.
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             Zhang,
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                                                                                                                                                             Napier, Mary A.
                                                                                                                                                                              Kljavin,Ivar J.
                                                                                                                                             Pan,James
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art, Timothy A.
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Roy, Margaret Ann
Stewart, Timothy 1
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Pan, James
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Kljavin, Ivar J.
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Goddard, Audrey
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Gerber, Hanspeter
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Botstein, David
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
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APPLICANT: Wood, William I.
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TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C2
CURRENT APPLICATION NUMBER: US/09/990,456
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Godowski, Paul J.
Grimaldi, J.Christopher
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Gerber, Hanspeter
                Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                 Gerritsen, Mary E.
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Ferrara, Napoleone
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Desnoyers, Luc
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Napier, Mary A.
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NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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APPLICANT: : Ashkenazi, Avi J.
: Baker, Kevin P.
: Botstein, David Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone US/09992598

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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-15
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/06511
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Sequence 424, Application US/
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Baton, Dan L.
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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2730P1C61

CURRENT APPLICATION NUMBER: US/09/989,735

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR PILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-17
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                                                                           LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE
                                                                                                                                       YLQDENENTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN
                       NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
                                                     LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVI
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CURRENT FILING DATE: 1097-06-16
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PRIOR APPLICATION NUMBER: 60/083322
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TITLE OF INVENTION: Secrete
TITLE OF INVENTION: Acids
FILE REFERENCE: P2730P1C19
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Desnoyers, Luc
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Stewart, Timothy
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Pan, James
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Grimaldi, J.Christopher
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
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APPLICATION NUMBER: US/09/991,181
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PRIOR APPLICATION NUMBER: 60/065250
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Kljavin, Ivar J.
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Query Match

Score 1253;

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Length 229;

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CURRENT FILING DATE: 2002-11-14
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PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-3
PRIOR PELING DATE: 1997-11-3
PRIOR PELING DATE: 1997-11-3
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PELING DATE: 1997-11-3
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR PELING DATE: 1998-03-20
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APPLICANT: Baker,Kevin p.
APPLICANT: Botstein,David
APPLICANT: Besnoyers,Luc
APPLICANT: Eaton,Dan L.
APPLICANT: Ferrara,Napole
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C11
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Botstein, David
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PR FILING DATE: 1998-07-01

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR PPLIORITION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR FILING DATE: 1998-02-25
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APPLICANT: Ashkenazi, Avi J.
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Botstein, David
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Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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APPLICATION NUMBER: 60/090472
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RESULT 23
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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TITLE OF INVENTION: Secreted and
TITLE OF INVENTION: Acids Encodi
FILE REFERENCE: P2730P1C38
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DR APPLICATION NUMBER: 60/091978
DR FILING DATE: 1998-07-07
SR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/92182
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APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/066770
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FILING DATE: 2001-11-15
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Eaton, Dan L.
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APPLICANT: Baker, Kevin F
APPLICANT: Botstein, Davi
FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Chas, Daniel
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Wood, William I
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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Pred. No. 4.1e-119;
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DR FILING DATE: 1998-06-02
PR APPLICATION NUMBER: 60/087827
DR FILING DATE: 1998-06-03
DR APPLICATION NUMBER: 60/089021
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/066770 APPLICATION NUMBER: 60/065311 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607 FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: 60/084600 FILING DATE: 1997-11-24 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: FILING DATE: 1998-06 FILING DATE: 1998-06 FILING DATE: 1998-06-APPLICATION NUMBER: 6
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APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532

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FILING DATE: 1998-06-17
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FILLING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246

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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembras
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C44
CURRENT APPLICATION NUMBER: US/09/997,428
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APPLICATION NUMBER: 60/091982
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091626
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Stewart,
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Kljavin, Ivar J.
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Grimaldi, J.Ch
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nilarity 99.6%;
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art, Timothy A.
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Pred. No. 4.1e-119;
0; Mismatches 1;
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APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25

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FILING DATE: 1998-00 APPLICATION NUMBER:

1998-06-24 1998-06-24

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APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:

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1998-06-24

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FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090435

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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24

CURRENT FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
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Paoni, Nargaret Ann
Roy, Margaret Ann
Stewart, Timothy A.
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Kljavin, Ivar J.
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Godowski, Paul
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PR APPLICATION NUMBER: 60/090429

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DR APPLICATION NUMBER: 60/091633

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DR APPLICATION NUMBER: 60/091978

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/991982

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/092182

DR FILING DATE: 1998-07-09

DR APPLICATION NUMBER: 60/092182

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Trans
TITLE OF INVENTION: Acids Encoding the FILE REFERENCE: P2730P1C3
CURRENT APPLICATION NUMBER: US/09/990
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Williams, P. Mick
Wood, William I.
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APPLICANT: Baker, Kevin F
APPLICANT: Botstein, Davi
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                                                             Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                           Baker, Kevin P
                Godowski,Paul J.
Grimaldi,J.Christopher
                                                 Goddard, Audrey
                                                                                              Fong, Sherman
                                                                                                               Ferrara, Napoleone
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Eaton, Dan L.
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Pan, James
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              Eaton, Dan L.
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Fong, Sherman
                                                                                                Baker, Kevin P.
Botstein, David
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APPLICANT: ZHOLD, ZEILEM
TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Scide Encoding the Same
FILE REFERENCE: P2730P1C2
CURRENT APPLICATION NUMBER: US/05/990,711
CURRENT PFILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/06570
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/083922
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The mas, Daniel
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Grimaldi, J. Christopher
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Goddard, Audrey
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Wood, William
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// GENERAL INFORMATION:
// APPLICANT: Askkenazi, Avi J.
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// APPLICANT: Botstein, David
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FILE REFERENCE: P2730P1C60
CURRENT APPLICATION UMBER: US/09/989,726
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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RESULT 31 US-09-998-156-424 ; Sequence 424, Application US/09938156

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Publication No. US20030044806A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730PlC28
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Gerritsen, Mary E
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Gurney, Austin L.
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art, Timothy A.
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FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-05 1998-06-1998-06-11 1998-06-1998-06-1 1998-06-13 1998-06-1998-06-1998-06-1998-06-05 1998-06-1998-06-10 1998-06-60/089440 60/089105 60/088861 60/088876 60/088826 9 60 9 60 60 60 60/088217 60/088212 60/088202 60/088167 60/088326 /088824 /088810 /088738 /088734 /088742 /088655

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                                              NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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US-09-990-437-424
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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR TILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/06511
PRIOR APPLICATION NUMBER: 60/06511
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PRIOR FILING DATE: 1997-11-13
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted at
TITLE OF INVENTION: Acids Ence
FILE REFERENCE: P2730P1C49
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OR APPLICATION NUMBER: 60/088212
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CURRENT APPLICATION NUMBER: US/09/91,157
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
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PRIOR PELING DATE: 1999-03-20
PRIOR APPLICATION NUMBER: 60/078910
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TITLE OF INVENTION: Secreta
TITLE OF INVENTION: Acids
FILE REFERENCE: P2730P1C51
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  OR APPLICATION NUMBER: 60/087827
OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/088021
OR FILING DATE: 1998-06-04
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Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/089948
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DR FILING DATE: 1998-06-17
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27309144
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087609
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087759
OR FILING DATE: 1998-06-02
OR FILING DATE: 1998-06-02
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FILING DATE: 1998-02-25
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
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etewart, Timothy
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Gerber, Hanspeter
Gerritsen, Mary E.
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Kljavin,Ivar J
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Eaton, Dan L.
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Botstein, David
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Sequence 424, Application US/03937573 Sequence 424, Application US/03937573 Publication No. US20030049682A1 Sequence 426, Application US/03937573 Publication No. US20030049682A1 Sepulcant Sequence 426, April J. Applicant Baker, Kevin P. Applicant Baker, Kevin P. Applicant Goddard, Andrey B. Applicant Rey, Margaret An. Applicant Pann, James P. Applicant Rey, Margaret An. Applicant Sewart Timethy A. Applicant Watanabe, Colin K. PRIOR PRIOR PRIVALENCE MARCHADA, Colon Marchada, Colin K. PRIOR PRIVALENCE MARCHADA, Colon Marchada, Colin K. PRIOR PRIVALENCE MARCHADA, Colon Marchada, Colin K. PRIOR PRIVALENCE MARCHADA,	QY I MODEDGYITLNIKTEKPALVSVGPASSFWWEVNALIILILCVGMVVGLVALGIWSVNORN 60 I MODEDGYITLNIKTEKPALVSVGPASSSWWEVNALIILILCVGMVVGLVALGIWSVXQRN 60 1 MODEDGYITLNIKTEKPALVSVGPASSSWWEVNALIILILCVGMVVGLVALGIWSVXQRN 60 QY 61 YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCJTNWRYYGDSCYGFFRHN 120 Db 61 YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCJTNWRYYGDSCYGFFRHN 120 QY 121 LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE 180 Db 121 LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE 180 QY 181 NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP 229 181 NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP 229
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Betsoyers, Luc
APPLICANT: Betson, Dan L.
APPLICANT: Ferrara, Napoleone
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PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
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FILE REFERENCE: P2730P1C16
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Stewart, Timothy A.
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TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C40
CURRENT APPLICATION NUMBER: US/09/997,559
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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Gerritsen, Mary E.
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Best 1
           APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C36

CURRENT APPLICATION NUMBER: US/09/997,601

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16
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DR APPLICATION NUMBER: 60/091544

DR FILLING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519

DR FILLING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091626

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Kljavin,Ivar J.
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                                                        LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE
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RESULT 40
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APPLICANT: Baker,Kevin p.
APPLICANT: Botstein,David
APPLICANT: Desnoyers,Luc
APPLICANT: Eston,Dan L.
APPLICANT: Ferrara,Napole
APPLICANT: Fong,Sherman
APPLICANT: Gerber,Hanspet
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A.
                                   Watanabe, Colin I Williams, P. Mick Wood, William I.
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FILE REFERENCE: P2730P1C12
CURRENT APPLICATION NUMBER: US/09/990,443
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250
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                                                          Paoni,
Watanabe,
           Stewart, Timo
Tumas, Daniel
                                                                                          Napier, Mary A.
                                                                                                         Gurney, Austin L
Kljavin, Ivar J.
                                                                                                                                        Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
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Gerritsen, Mary E.
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                                           Margaret Ann
                                                            Nicholas F.
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                          Timothy A.
Colin K.
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/991,854
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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OR FILING DATE: 1998-06-04
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Sequence 424, Application US/0
Publication No. US20030059782A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Bester Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary Z.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Johnist
APPLICANT: Goddard, Johnist
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
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Goddwski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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FILE REFERENCE: P2730FIC30

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CURRENT PLING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1997-10-17

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Gerritsen, Mary
Goddard, Audrey
Godowski, Paul -
                                               Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
                                                                                                     Baker, Kevin P.
Botstein, David
                                      Gerber, Hanspeter
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PZ730P1C32
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OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/0
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Kljavin, Ivar J
Napier, Mary A.
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GENERAL INFORMATION:
APPLICANT: ABREACA, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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               Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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FILE REFERENCE : P2730PICS9

CURRENT APPLICATION NUMBER: US/09/989,729A

CURRENT PILING DATE: 1997-06-16

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REFERENCE: P2730P1C59
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Grimaldi,J.Christopher
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Sequence 424, Application US/09997349
publication No. US20030059832A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Botstein, David
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YLQDENENRTGTLQQLAKRFCQYVVKQSBLKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN 120
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                                            LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE
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US-09-990-440-424
; Sequence 424, Application US/09990440
; Sequence 420, Application US/0990440
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and T.
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730P1C21
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Baker, Kevin P
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Stewart, Timothy
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Score 1253; DB 11;
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TITLE OF INVENTION: Secreted and Transmembrai TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730FICS: CURRENT APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 2001-11-14 PRIOR PRIOR PLILING DATE: 1997-0-17 PRIOR APPLICATION NUMBER: 60/06250 PRIOR APPLICATION NUMBER: 60/06250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/065186 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 60/065311 PRIOR FILING DATE: 1997-11-13 PRIOR FILING DATE: 1997-11-13 PRIOR FILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/06670 PRIOR FILING DATE: 1997-11-24 PRIOR APPLICATION NUMBER: 60/0675945 PRIOR FILING DATE: 1998-02-25 PRIOR FILING DATE: 1998-02-25 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/08332 PRIOR APPLICATION NUMBER: 60/08332 PRIOR APPLICATION NUMBER: 60/08332 PRIOR APPLICATION NUMBER: 60/087106 PRIOR FILING DATE: 1998-04-28 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/08707 PRIOR FILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087607 PRIOR APPLICATION NUMBER: 60/087607 PRIOR APPLICATION NUMBER: 60/087607 PRIOR PRILING DATE: 1998-06-02 PRIOR APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087609 PRIOR APPLICATION NUMBER: 60/087759 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 PRIOR APPLICATION NUMBER: 60/087827 
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Gerritsen, Marry E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Ferrara, Napoleone
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P. Mickey
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Query Match Best Local Similarity

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                    This sequence represents a human secreted protein of the invention. The extended CDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against proteins encoded by the extended cDNAs are useful in identification of this tissue types or cell species, as well as identifying tissue specification of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
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Best I
                                                                                                                                                                                                                                                                                                                                                                                                                                               identification of genes associated with hereditary diseases or drug response. signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
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                                                                                                         NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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98US-0088030.
98US-0088030.
98US-0088033.
98US-0088206.
98US-0088202.
98US-0088212.
98US-0088272.
98US-0088272. 98US-0088655. 98US-0088722. 98US-0088730. polypeptide; PRO polypeptide; LDL receptor; TIE ligand; receptor immunoadhesin; gene mapping. protein PR01384 98US-0088021 98US-0088025 98US-0087607 99WO-US12252 -0087827 -0087759 entry.

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10-JUN-1998; 10-JUN-1998; 10-JUN-1998;

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S-0088741. S-0088742. S-0088810. S-0088811.

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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant rechairms.
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16-DEC-1999;
20-DEC-1999;
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24-FEB-2000;
21-MAR-2000;
21-MAR-2000;
31-MAR-2000;
31-MAR-2000;
22-MAR-2000;
22-MAY-2000;
30-MAY-2000;
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11-FEB-2000;
18-FEB-2000;
18-FEB-2000;
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02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
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N-2000; 2000WO-US00376.
BB-2000; 2000WO-US03565.
BB-2000; 2000WO-US04341.
BB-2000; 2000WO-US04341.
BB-2000; 2000WO-US04914.
BB-2000; 2000WO-US0504.
NR-2000; 2000WO-US05004.
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NR-2000; 2000WO-US04442.
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99WO-US30911.
99WO-US30999.
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99US-0170262.
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Pred. No. 6.5e-119;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO; mammalian; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
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TNF-alpha;
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                                                                                                                                                                                                                                                                                                                                ANUI2172-ANUI2446 represent movel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC polypeptides, and to detect the presence of mammalian lung, colon, CC polypeptides, and to detect the presence of mammalian lung, colon, CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of cumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or cartilage, the proliferation of inner ear utricular supporting cells or cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood concoytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide colors involved in binding interactions. The polymplocytes enable used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated, secretory and transmembrane PRO polypeptide used to other PRO polypeptides, link bioactive molecules to cells expr PRO polypeptides, and detect the presence of mammalian functure lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerritsen ME,
Smith V, Stew
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                                                                                                                                                                                                                                                                                                     Sequence
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                               LTWEESKQYCTDMNATLLKIDNSNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE
                                                                         YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN
                                                                                                         YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGJSCYGFFRHN
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Tumas D,
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A, Godowski
                                                                                                                                                                                                                             0
                                                                                                                                                                                                                           Score 1253; DB 22;
Pred. No. 6.5e-119;
0; Mismatches 1;
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RESULT 4
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ID AAB6
XX
AC AAB6
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DE Huma
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KW Huma
KW Cell
Human; secreted cell death; canc
                           Human PRO1384 (UNQ721)
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                                                                                AAB65288
                                                                                standard;
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                                                                                Protein;
                           protein sequence
                                                                                 AA
         protein;
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and transmembrane cer; chromosomal ma

mapping; gene

PRO;

mapping; tissue

typing;

181

NMFEELEDGKGNMNCAYFHNGKMHPTFCBNKHYLMCERKAGMTKVDQLP

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Query Match
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Matches 228;
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11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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28-JUL-1999;
17-AUG-1999;
                                                                                                                                                                                                        The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as texins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating causer. Anti-PRO antibodies can be used in diagnostic assays. ARF44770 to ARF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44070 to AAF44269 and AAB65100 represent human PRO polynucleotide and protein sequences are the processing the processing the processing the processing and the processing processing the processing processing the processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing processing process
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Ferrara N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Fig 306; 935pp; English.
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DB; AAF44257.
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                                                                     Similarity
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2000WC-US00219
2000WC-US00376
2000WC-US03365
2000WC-US04341
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99WO-US28301.
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99WO-US21547.
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99US-0143048.
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                               Score 1253; DI
Pred. No. 6.5e
0; Mismatches
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Godowski E
Paoni NF;
Wood WI;
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12-JUN-1998;
14-JUL-1998;
28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO polypeptide; secreted and transmembrane protein; tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; differentiation; chondrocyte; tumour; genetic disorder;
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Smith V,
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ME, Goddard A, Godo
Stewart TA, Tumas D,
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A, Godowski PJ, Gurney AL,
        Watanabe CK,
        Wood WI,
                   Filvaroff E,
L, Sherwood S;
        Zhang
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         US2003032155-A1
                             Homo sapiens
                                                 bioreactor;
                                                                                        Human; secreted protein; transmembrane
                                                                                                                                 27-MAY-2003
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REPRESENTED IN TO THE PROPERTIES AND THE PROPERTIES

The present invention relates to the isolation of novel human PRO CC polypeptides, and the polymucleotide sequences encoding them. The CR PRO polypeptides are useful for detecting other PRO polypeptides, for clinking bloactive molecules to cells expressing PRO polypeptides, for clinking bloactive molecules to cells expressing PRO polypeptides, for for modulating biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the propeptides are useful for the muman blood, for stimulating the presence of tumours. The polymucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and copylogopides are useful as hybridisation probes, in chromosome and copylogopides are useful as hybridisation probes, in chromosome and copylogopides are useful as hybridisation probes, in chromosome and copylogopides, and in gene therapy. ABU6670-ABU66844 represent the human copylogopides of the invention.

CC disorders, and in gene therapy. ABU66874 represent the human copylogopides of the invention.

CC polypeptides are useful as hybridisation with genetic copylogopides of the invention.

CC format directly from the USPTO web site at CC sequence data for this patent was obtained in electronic copylogopides. New secreted and transmembrane PRO nucleic acids, usefutherapy, in chromosome and gene mapping, as chromosome tissue typing, and in chromosome identification -Claim 12; Fig 522; 660pp; English useful markers, for gene ers, in

MQDBDGYITLNIKTRKPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRN NMFEFLEDGKGNMNCAYFHNGKMIPTFCENKHYLMCERKAGMTKVDQLP NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQXSNEVWKWEDGSVISE LTWEESKQYCTDMMATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE YLQDENENRIGILQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRN YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN Conservative 99.4%; Score 1253; DB 24; Pred. No. 6.5e-119; Length 229; Indels 222 229 .. O Sass 60 180 180 120 120 9

Protein; 229

Human secreted/transmembrane, PRO, protein SEQ ID 522

įntein; PRO;

inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defects; premature aging; AIDS; biosensor; acquired immunodeficiency syndrome; cancer; diabetic complication;

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WPI; 2003-331925/31. N-PSDB; ACA04284.

atherosclerosis, cardia aging, AIDS, or cancer designated secreted and transmembrane nucleic acids and polypeptides, ignated as PRO, useful for treating inflammation, organ failure, eroscleosis, cardiac injury, infertility, birth defects, premature

Claim 12; 5,5 522; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is CC at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide CC (one of 275 secreted or transmembrane proteins). The nucleic acid CC under American Type Culture Collection (ATCC) accession number in a list CC given in the specification. Also included are vectors and host CC given in the specification. Also included are vectors and host CC cells for producing PRO proteins, methods for stimulating the release of CC TNF-alpha (tumour necrosis factor alpha) from human blood, CC antibodies, PRO extracellular domains and mature sequences, methods CC in the proliferation of differentiation of chondrocyte cells, the proliferation of of sectors alpha) from human blood, CC and the proliferation of differentiation of inner ear unticular CC supporting cells, the proliferation of representation of inner ear unticular CC supporting cells, the proliferation of relymphocyte cells, the release or G1 success or free factor MIA, a method for modulating the uptake CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the CC proliferation of endothelial cells), a method for modulating the uptake CC or the differentiation of adipocyte cells, a method for detecting the collypeptides are useful for treating inflammatory diseases, organ CC premature arise and all control inflammatory diseases, organ CC promature are useful for treating inflammatory diseases, organ control and control of c premature diabetic (atherosclerosis, cardiac injury, infertility, birth e aging, AIDS (acquired immunodeficiency syndrome), c ne), cancer, or hybridisation

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PR 14-1
PR 12-1
PR 12-1
PR 11-1
PR 1
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 14-SEP1998
16-SEP1998
16-SEP1998
17-SEP1998
07-OCT1998
29-OCT1998
29-OCT1998
29-OCT1998
29-OCT1998
01-DEC1998
01-DEC1998
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                                                                                                                                                                                      12-JUN-1998;
14-JUL-1998;
28-AUG-1998;
10-SEP-1998;
14-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; PRO; hypertrophy of neonatal heart; angiogenesis; would healing; cardiac insufficiency disorder; carcer; tumour; immune response; adrenal cortical capillary endothelial growth; -fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum, kidney disorder; mammallan kidney mesangial cell proliferation; Berger disease; denondrocyte proliferation; sports injury; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-2003
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                                                                                                                                                                                                                                                                                       31-MAR-1997;
                                                                                                                                                                                                                                                                                                                             07-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein; 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMFBFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLQDENENRIGILQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 AA;
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                                                                         98WO-US12456.

98WO-US14552.

98WO-US1888.

98WO-US19093.

98WO-US19077.

98WO-US19177.

98WO-US19177.

98WO-US191330.

98WO-US19330.

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   )-US22992.
)-US24855.
)-US25108.
)-US00106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1253; DB 24;
Pred. No. 6.5e-119;
0; Mismatches 1;
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       08-MAR-1999
20-MAR-1999
21-SEP-1999
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13-SEP-1999
13-SEP-1999
15-SEP-1999
15-SEP-1999
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29-NOV-1999
20-DEC-1999
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99WO-US28551

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99WO-US3091

99WO-US3072

99WO-US31243

99WO-US31274

2000WO-US01277

2000WO-US01277

2000WO-US01274

2000WO-US01274

2000WO-US0131441

2000WO-US0131441

2000WO-US051461

2000WO-US051461

2000WO-US051461

2000WO-US053141
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2000WO-US06319.

2000WO-US06884.

2000WO-US07377.

2000WO-US07532.

2000WO-US08439.

2000WO-US13705.

2000WO-US14042.

2000WO-US14941.
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2001WO-US06666.
2001WO-US17092.
2001WC-US17800.
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2000WO-US20710.
2000WO-US22031.
2000WO-US23522.
       2001WO-US19692.

2001WO-US21066.

2001WO-US21735.

2001WO-US21735.

2001US-0796498.

2001US-0802706.

2001US-0808689.

2001US-081744.

2001US-081744.

2001US-0854280.

2001US-0854280.

2001US-08560216.

2001US-08660216.
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2000WO-
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99WO-US20594.
99WO-US20944.
99WO-US21090.
99WO-US21547.
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)-US12252.
)-US20111.
)-US20594.
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0-US30952.
0-US30873.
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                                                                                                                                                                                                                                                                   Query Match
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21-JUN-2001;
18-JUL-2001;
06-AUG-2001;
09-AUG-2001;
16-AUG-2001;
19-DBC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001;
05-JUN-2001;
14-JUN-2001;
                                                                                                                                                                                                                                                                                                                                               disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO134 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 522; 659pp; English.
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                                                                                                                                                                                                                                                  Local
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                                                                 YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFREN
                                                                                                     YLQDENENRIGILQQLAKRFCQYVVKQSELKGIFKGHXCSPCDINWRYYGDSCYGFFRHN
                                                                                                                                             MODEDGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRN
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ME, Goddard
                                                                                                                                                                                                                                                                                                           229 AA;
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; 2001US-0886342.

; 2001US-0887879.

; 2001US-0908827.

; 2001US-0927419.

; 2001US-0927796.

; 2001US-0921836.

; 2001US-0921836.
                                                                                                                                                                                                                             Conservative
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2001US-0874503.
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Tumas D,
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, Godowski PJ, Gurney AL,
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No. 6.5e-119;
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AL, Sherwood S;
lood WI, Zhang Z;
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02-JUN-2000;
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11-AUG-2000;
23-AUG-2000;
24-AUG-2000;
08-NOV-2000;
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22-MAY-2000;
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30-MAR-2000;
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                                              2000WO-US20710.
2000WO-US22031.
2000WO-US23522.
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2000WO-US14042.
2000WO-US14941.
2000WO-US15264.
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2000WO-US05004.
2000WO-US05841.
2000WO-US06319.
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2000WO-US04341.
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2000WO-US08439.
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2000WO-US00376
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98WO-US25108.
99WO-US00106.
99WO-US05028.
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99WO-US28301.
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98WO-US19437
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01-DEC-2000;
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29-JUN-2001;
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17-OCT-1997;
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Ferrara N, F
Grimaldi JC,
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04-JUN-1998;
               Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
                                                                                    Grimaldi
Roy MA,
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                                                                                                                              GENENTECH INC.
                                                                                    Stewart
                                                                                   AJ, Baker KP, Botstein D, Desnoyers L, Eston, Fong S, Gerber H, Gerriteen ME, Goddard A, UC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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2001WO-US06520.
2001WO-US17800.
2001WO-US19692.
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2001WO-US21735.
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97US-065186P.
97US-065311P.
97US-065311P.
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97US-0670P.
98US-075945P.
98US-078910P.
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98US-088167P
98US-088127P
98US-088217P
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     Best Loc
Matches
                                   antibody-dependent enzyme mediated
                                            Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy; tumour-associated antigenic target; TAT;
     US2003027162-A1
                    Homo sapiens
                                                                             Human
                                                                                              22-APR-2003
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                                                                             secreted/transmembrane protein,
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standard;

Protein;

229 B

(first

entry)

#171.

prodrug

therapy; cytostatic.

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CC PRO136 and pRO1387 induce o-fos in endothelial cells, and are thus consequently the properties of this polypeptide are consequently for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are cuseful for treating cancerous tumours. PRO812 inhibits vascular cells and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting endothelial cell growth in cells and is thus useful for inhibiting throur growth. PRO826, PRO168, PRO1184, PRO1346 and PRO1375 stimulate proliferation of endothelial cells which would be beneficial in inhibiting throur growth. PRO826, PRO168, PRO1184, PRO1346 and PRO1375 stimulate proliferation of certinal neurons cells (PRO1132 is also enhances survival/proliferation of crod photoreceptor cells) and therefore are useful for treating retinal cell disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813, PRO813 cand therefore are useful for treating thing wesangial cells (and therefore are useful for treating thing providers associated with decreased mesangial cell function such as Berger disease or other caphropathies associated with dermeatitis, herpetiformis or Crohn's cellsease. PRO1310, PRO844, PRO1312, PRO1122 and PRO1387 induce the comparation and/or redifferentiation of chondrocytes in culture and certain useful for treating sports injuries, and arthritis. This certain amino acid sequence of a novel human PRO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
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                                                     NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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NMFEELEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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Se-119;
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PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; insufficiency disorder; cancer; tumour; immune response; cortical capillary endothelial growth; c-fos induction;
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vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.

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25-FEB-1998
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                                                        polymuclectides are also useful in gene therapy, in chromosome polymuclectides are also useful in gene therapy, in chromosome polymetrication, as chromosome markers, or in generating probes. The PRO polymetrides are useful as molecular markers for protein electrophoresis, and the isolated mucleic acids may be used for recombinantly expressing those markers. The PRO polymetrides and nucleic acids may also be used in tissue typing, Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ABUG0478-ABUG0624 are the PRO polymucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eg
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddaard
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams
                                                                                                                                                                                 The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or
                                                                                                                                                                                                                                                                                 New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, chromosome markers, or in generating probes -
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Eaton M. A.

Paoni Wood Godowski

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11-DEC-1999;
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28-WAY-1998;
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Matches 228
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C7-JUL-1999;
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colon cancer; lung
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nilarity 99.6%;
Conservative
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99WO-US30095.
99WO-US30911.
2000WO-US00219.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
2000WO-US04414.
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17-OCT-1997;
12-NCV-1997;
13-NOV-1997;
24-NOV-1997;
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            Ashkenazi A
Ferrara N,
Grimaldi JC
Roy MA, St
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            i AJ, Baker KP, Botstein D, Desnoyers L, Eaton
N, Fong S, Gerber H, Gerritsen ME, Goddard A,
JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Stewart TA, Tumas D, Watanabe CK, Williams PM,
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RESULT 14
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Best Local
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                                                                                                                                                                    Human PRO1384 polypeptide
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    97WO-US20069
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polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, catts, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or meNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABU58900-ABU59046 are the PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancers (e.g. lung or breast cancers), or for diagnosing these cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig 306; 647pp; English
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NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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                                                                   NMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
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Pred. No. 6.5e-119;
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16-SEP-1998;
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07-OCT-1998;
01-DEC-1998;
05-JAN-1999;
08-WAR-1999;
15-SEP-1999;
15-SEP-1999;
15-SEP-1999;
16-DEC-1999;
01-DEC-1999;
01-DEC-1999;
16-DEC-1999;
16-DE

98WO-US19437 98WO-US21141 98WO-US21141 98WO-US25108 99WO-US25028 99WO-US25028 99WO-US21592 99WO-US21547 99WO-US23313 99WO-US23313 99WO-US28313

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CC polypeptides, and the polymucleotide sequences encoding them. The CC prolypeptides are secreted and transmembrane proteins. The PRO CC prolypeptides are useful for detecting other PRO polypeptides, for CC linking bloactive molecules to cells expressing PRO polypeptides, for CC linking bloactive molecules to cells expressing PRO polypeptides, for CC polypeptides, and for for identifying agonists or antagonists. CC polypeptides, and for for identifying agonists or antagonists. CC polypeptides, and for for identifying agonists or antagonists. CC polypeptides, and for for monosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for CC generating transgenic animals or knockout animals, to construct CC phyridisation probes for mapping the gene which encodes the PRO cC disorders, in gene therapy, for chromosome identification, as CC disorders, in gene therapy, for chromosome identification, as CC chromosome markers, and for generating probes for PCR, Northern CC chromosome markers, and for generating probes for PCR, Northern CC crace in the sequence data for this patent was obtained in electronic format directly from the USFTO web site at CC sequate uspro-gov/psipsbIDEntry.html.
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Grimaldi JC,
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Zhang Z;
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28-AUG-2001;
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17-JUN-1998;
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                                                                                                                                                                    Similarity
                                                                                                          MQDEDGYITLNIKTRKDALVSVGPASSEWWRVMALILLILCVGMVVGLVALGIWSVMQRN
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                                                         YLQDENENRIGILQQLAKRECQYVVKQSELKGIFKGHKCSECUTNWRYYGDSCYGFFRHN
                                                                                         modeddyitiniktrkpalvsvopassswikvmalilliicvomvvolvaloimsvmorn
                              YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHN
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98US-08916P

98US-089140P

98US-089514P

98US-089514P

98US-089512P

98US-089532P

98US-089538P

98US-089598P

98US-089598P

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98US-08960P
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                                                                                                                                                       Conservative
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Pred. No. 6.5e
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08-NOV-2000; 24-AUG-2000;

20-JUN-2001; 29-JUN-2001;

11-AUG-2000; 23-AUG-2000; 02-JUN-2000; 28-JUL-2000; 22-MAY-2000; 30-MAY-2000; 15-MAR-2000; 20-MAR-2000;

10-MAR-2000;

15-MAY-2000; 17-MAY-2000;

99WO-US30911
2000WO-US00376
2000WO-US00376
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2001WO-US217360
2001WO-US21735

09-JUL-2001; 16-JUN-1997; 17-OCT-1997; 12-NOV-1997; 13-NOV-1997;

97US-066770P. 98US-075945P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMFBFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCBRKAGMTKVDQLP
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2000WO-US034341.
2000WO-US04914.
2000WO-US05004.
2000WO-US05004.
2000WO-US050841.
2000WO-US050841.
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2000WO-US23528.
2000WO-US23528.
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2001WO-US35620.
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         Ashkenazi A. Fc. Perrara N, Fc. Gui...
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25-FEB-1998

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07-MAY-1998

07-MAY-1998

07-JUN-1998

07-J
    The invention relates to a secreted and transmembrane polypeptide, te PRO polypeptide, and the polynucleotide encoding it. The polypeptide useful for detecting PRO polypeptides and for linking a bioactive molecule to a cell expressing the above polypeptides, where the bioac
                                                                                                                                                            Novel secreted and activity of cell exantagonists of poly
                                                                                                                                                                                                                                                        WPI; 2003-066810/06.
N-PSDB; ABX17181.
                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                             AJ, Baker KP, Botstein D, Desnoyers L, Eaton, Fong S, Gerber H, Gerritsen ME, Goddard A, JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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97US-062350P

97US-065311P

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98US-075945P

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                                                                                                                      306;
                                                                                                                                                              ll expressing polypeptide,
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                                                                                                                                                                transmembrane polypeptide expressing the polypeptide, ypeptide, and as molecular
                                                                                                                   4dg559
                                                                                                                      English
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Godowski PJ
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Matches 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome identification, as a chromosome marker and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. This sequence represents a human PRO polypeptide of the
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                                                                                                                                                                                                                                                                                             wound; burn; ulcer; Alzheimer's amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                Neuroprotective; immunomodulator; cancer; chromosome 12; cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
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WPI; 2002-426278/45.
N-PSDB; ABQ60831.
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                                              Liu
Yang
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                                                Zhou P,
Wehrman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral solerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABB43989 represent polypeptides encoded by polynucleotides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary, neuroprotective, immunomodulator, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID # 490; 357pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: The sequence data for this patent did not form specification, but was obtained in electronic format
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                              10-AUG-2001; 2001US-311305P.
24-AUG-2001; 2001US-314734P.
07-SEP-2001; 2001US-318204P.
01-OCT-2001; 2001US-326470P.
                                                                                                                                                                                                                                                                           Human GENSET
                                                                                                                                                                             WO2003014151-A2
                                                                                                                                                                                                                                            GENSET; cytostatic;
                                                                                                                                                                                                                                                                                                           12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                             ABR39424 standard; protein; 229
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                                                                                                                15-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to 446 newly isolated polynucleotide sequences activity of polynucleotides of the invention may be described as
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                                                                                                                                                                                                                                                                           polypeptide clone name Lectir
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein; TANGO 269; clone jthAa35c12; chromosome 12; type II transmembrane protein; LOX-1; OXLDL; splenic disorder; textin-like oxidised low density lipoprotein receptor; addrenal disorder; liver disorder; blood and haematopoietic associated disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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/note= "(
106..113
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43..48
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99..10
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14..16
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                                                                                                                                                    Mature_TANGO_269
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Pred. No. 4
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                         kinase II
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t.2e-118;
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                                                                                                                                                                                                                                                                                                                                 The present sequence representing a novel human secreted protein TANGO 269 is isolated from clone jthAa35c12 from a human adrenal gland cDNA library. The gene encoding TANGO 269 is found to map to chromosome 12. TANGO 269 which is a type II transmembrane protein shows sequence homology to human lectin-like oxidised low density lipoprotein receptor (LOX-1). TANGO 269 may bind oxidised low density lipoprotein (OXLDL) to modulate the pathway. TANGO 269 may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                         treat adrenal disorders (e.g. hypoadrenalism), liver disorders (e.g. cirrhosis), bone marrow, blood and haematopoletic associated disorders (e.g. leukaemia), splenic disorders (e.g. splenomegally), cardiovascular disorders (e.g. schaemic heart disease, atherosclerosis), immune disorders (e.g. arthritis, AIDS), inflammatory disorders (e.g. asthma), TNF-alpha related disorders (e.g. acute myocarditis) and platelet disorders (e.g. thrombosis). The invention also describes the novel secreted proteins murine TANGO 269 (AAU02496) and human TANGO 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rucleic acid molecule encoding useful for treating immune related
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17-MAY-2000; 2000US-0572275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser CC,
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                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM
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121 LTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISE
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                                                                                                                                                 Similarity
                                                   YLQDENENRTGTLQQLAKRFCQYVVKQSBLKGTFKGHKCSPCDTNWRYYGDSCYGFFREN
                                                                                                    MQDEDGYITLNIKTRKPALVSVGPASSFWWRVMALILLLILCVGWVVGLVALGIWSVMQRN
                           YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTF
                                                                               MQDBDGYITLNIKTRKEALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRN
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                                                                                                                                   Conservative
                                                                                                                                                                                        AA;
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/note= "(
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205..208
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133..136
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174..179
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127..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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                                                                                                                                               97.7%;
98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           English
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                                                                                                                                   Score 1231.5; DB 2:
Pred. No. 9.8e-117;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; artiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection
           AAM25963. The proteins can have activities based on the tissues and cells they are expressed in such as antiinflammatory; antirhumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide; anti-HIV, fungicide; antiasthmatic; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidabetic; cycostatic; neuroprotective; antidapressant; noctropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, neuroptote shock, pancreatitis, cardiac dysfunction, representation, septic shock, pancreatitis, cardiac dysfunction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM25751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000;
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neuropathology, cardiac anaphylaxis,
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                                                                                                                                                                                                                                                                                                                                                                                          AAH99692.
                                                                                                                                                                                                                                                                                                                                human polynucleotides encoding polypeptides, useful for t and diagnosis of e.g. cancer, ulcers and HIV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                               Page 263; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 99US-0471275.
; 2000US-0488725.
; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder.
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 viral,
bacterial, HIV
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Best Local :
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                                                                                                                                                                                                                                                                                                                         Mus
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                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                   cardiovascular
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                                                                                                                                                                                                                                                                                                                                                                                                                         Murine secreted protein TANGO
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                                                                                                                                                                                                                                                                                                                                                    disorder; inflammatory disorder; immune
   /note= "As: __ _
122..125
/note= "Casein kinase II phosphorylation
                                                                                                                                     /note=
93..96
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107..1
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/label= Mature_TANGO_269
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                                                                         'label= Extracellular_link_domain
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Pred. No. 9.8e-115;
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                                                                                                                                                  kinase
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                                                                                                                                                                                                                                                                                                                                                                    The present sequence representing a novel murine secreted protein TANGO 269 is isolated from clone jtmea040e07 from a mouse megakaryocyte CDNA library. Human TANGO 269 (AAU02495) is also described. TANGO 269 which is a type II transmembrane protein shows sequence homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-OCT-1999;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-OCT-2000; 2000WO-US29797
                                                                                                                                                                                                                                                Teukaemia), splenic disorders (e.g. splenomegaly), cardiovascular disorders (e.g. ischaemic heart disease, atherosclerosis), immune disorders (e.g. arthritis, AIDS), inflammatory disorders (e.g. bact infection), TNF-alpha related disorders (e.g. acute myocardiis) and platelet disorders (e.g. thrombosis). The invention also describes
                                                                                                                                                                                                                                                                                                              which is a type II transmembrane protein shows sequence homology to human lectin-like oxidised low density lipoprotein receptor (LOX-1). This may bind oxidised low density lipoprotein (OXDL) to modulate the pathway. TANGO 269 may be used to liver disorders (e.g. cirrhosis), blood and haematopoietic associated disorders (e.g. cirrhosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAY-2001
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                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid molecule encoding type II transmembrane proteins ful for treating immune related disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                    secreted
                                            60
                                                                     61
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20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS04268
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 6; 137pp;
HNLTWBESKQYCTDMNATLLKIDNRNIVEYIKARIHLIRWVGLSRQKSNEVWKWEDGSVI
                                                                                                                        MQDEDGYITLNIKTRKPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRN
                                            YLLAEKENLSATLOOLAKKSCOELIROSEIKTKSTFB-HKCSPCATKWRYHGDSCYGFFR
                                                                     YLQDENENRTGTLQQLAKRFCQYVVKQSEL--KGTFKGHKCSPCDTNWRYYGDSCYGFFR
                                                                                                MODEDGYITLNIKPRKQALSSAEPASS-WWRVAALVILISSMGLVVGLVALGIMSVTQQK
                                                                                                                                                                                                         229
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0572275
                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                   protein
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182..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Casein kinase II phosphorylation
223..226
/note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
207..21
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207..2
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                                                                                                                                                                                                                                    (e.g. thrombosis).
ein human TANGO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .210
e= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .187
                                                                                                                                                  61.5%; Score 776; DB 22; 63.0%; Pred. No. 1.8e-70; tive 31; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Casein kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase C phosphorylation
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                                                                                                                                                                                                                                      298
                                                                                                                                                                                                                                       (AAU02497).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation
                                                                                                                                                                              Length 229;
                                                                                                                                                        Indels
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RASULT 21
AAYC5317
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XX Secretary Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is a human secreted protein of the invention. The secreted proteins were obtained from human adult placenta, foetal brain, adult testes or adult blood cDNA libraries. The polynucleotides (PNs) and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemacopoiesis regulating activity, tissue growth activity, activity, haemacopoiesis regulating chemotactic/chemokinetic activity, activity and thrombolytic activity, chemostatic and thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; human; nutritional activity; cytokine; tissue growth; cell proliferation; cell differentiation; immune stimulant; chemotaxis; immune suppressant; haematopoiesis regulator; activin; inhibin; cadherin; chemokinesis; haemostasis; thrombolysis; anti-inflammatory; gene therapy; tumour invasion suppressor; tumour inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino
Merberg D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05317 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WC9913066-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                             chemotactic/chemokinetic activity, haemostatic and thrombolytic activity receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The PNs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                          Sequence
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DB; AAX33810.
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                                                                                                                MLDDÓGDTTMSLHSQASATTRHPEPRRTEHRAPŚSTWRPVALTLLTLCLVLLIGLAALGL
                                                                                                                                                                     MODEDGYITLNIKTRKPALV-----SVGPASSFWWRVMALILLILCVGMVVGLVALGI
LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J, Evans C,
Racie LA,
                                                                                                                                                                                                                                                                                                                                             280
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                                                                                                                                                                                                                                   Conservative
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Spaulding V,
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                                                                 SVMQRNY-
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                                                                                                                                                                                                                                                           Score 352.5; DB 20; Pred. No. 2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      therapy.
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                                                              -LQDENENRTGTLQQLAKRFCQYVVKQSE
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RESULT 22
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02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus exthematosus; infection; cholesterol ester storage; systemic lupus exthematosus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressint; cardiant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB42619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                            AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatocropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000WO-US08621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                 immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                          useful for treatin
                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200058473-A2
                                                                                                                                               Claim
                                                                                                                                                                                                              Novel
                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                              Shimkets RA,
 antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                                                              (CURA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                               2000-602362/57
                                                                                                                                                                            nucleic acids and peptides derived from open reading 1 for treating e.g. cancers, proliferative disorders, degenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTFFTSELFHIIDVTSFRSRDCVAILNGMI
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                                                                                                                                                                                                                                                                                                                              CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | LKGTFKGHKGSPCDINWRYYGDSCYGFFRHNLTWBESKQYCTDDNATLLKIDNRNIVEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ombined immunodeficiency; malaria; autoimmune disorder; asthma; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; age; cartilage damage; antlinflammatory disease; ccagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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2000US-0540763.
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        antirheumatic;
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RESULT 23
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), ADDS, viral,
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                                                                                                                                                                                                                                                                        polypeptide; PRO polypeptide;
 98US-00877697.
98US-0087759.
98US-0087727.
98US-00887827.
98US-00880221.
98US-0088022.
98US-0088029.
98US-0088033.
98US-0088033.
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11-AUG-1998

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N-PSDB;
The invention provides membrane-bound PRO polypeptides and polymucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents to bit receptor-ligand interactions. The membrane-bound proteins can also be
                                                                                                                            Membrane-bound proteins and related nucleotide
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                                                                                                        claim
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DB; AAZ65072.
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98US-0091978.
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98US-0095282.
98US-0095321.
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4-1998; 4-1998; 4-1998;

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98US-0088167 98US-0088212 98US-0088217 98US-0088730 98US-0088730 98US-0088740 98US-0088741 98US-0088874 98US-008881 98US-0088861 98US-00888626 98US-0088863 98US-0089512 98US-0089512 98US-0089512 98US-0089512 98US-0089512 98US-0089514 98US-0089512 98US-0089514 98US-0089514 98US-0089514 98US-0089514 98US-0089514 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-008953 98US-0089947 98US-0090254 98US-0090254 98US-009035 98US-009035 98US-0090431 98US-0090444 98US-0090444

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Best Local
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                                                                                                                                                                                                                                                                                                          Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina; cardiovascular disease; lipid metabolism; myocardial infarction; cerebral ischaemia; arterial thrombosis; thrombotytic; antilipaemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE11932
                                                            14-APR-2000; 2000US-1971372.
20-JUN-2000; 2000US-0598042.
32-AUG-2000; 2000US-0631451.
22-SEP-2000; 2000US-0667298.
17-NOV-2000; 2000US-0714936.
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                neuroprotectant; cerebroprotective;
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Ballinger DG,
Liu C, Asundi
                                                                                                                                                                     25-OCT-2001
                                                                                                                                                                                             WO200179446-A2
                                                                                                                                                                                                                                   Domain
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 Montgomery JR,
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                                                                                                                                                                                                                                                                                                    variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3e-27;
nes 92;
  Tang TY,
Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LODENENRTGTLOOLAKRFCQYVVKQSE
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    Zhou
RT, F
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     Ren F,
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                Goodrich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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Query Match Best Local

28.0%; 29.1%;

22;

Length

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cc and protein sequences are useful for treating or preventing disorders can protein sequences are useful for treating or preventing disorders can acciated with apolipoproteins, lipases and lipoprotein receptor (ALLY) cexpression and for treating lipid metabolism, cardiovascular diseases and thrombosis. Antibodies against these proteins are useful for cardiovascular diseases and the presence of or predisposition to a disease associated with altered levels of these sequences. ALLY polypeptides are also cuseful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALLY proteins are useful for identifying a constraint expression or physiological interactions of this polypeptide. Cc aberrant expression or physiological interactions of this polypeptide. Cc producing ALLY proteins. The nucleic acids and polypeptides of the convention are also useful for the treatment of occlusive cardiovascular cdiseases, mycardial infarction, cerebral ischaemia, anglina, arterial conventions of the invention are also useful for the treatment of occlusive cardiovascular chrombosis, coronary artery thrombosis and cerebral artery thrombosis of the invention are also useful for the treatment of occlusive cardiovascular chrombosis, coronary artery thrombosis and cerebral artery thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides encoding proteins CG122, CG179, CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins involved in lipid metabolism and cardiovascular disease such as human apolipoproteins, lipases and lipoprotein receptor proteins. These DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human apolipoproteins, lipases, and lipoproteceptor polypeptides, useful for preventing diagnosing and treatilipid metabolism disorders, thrombosis and cardiovascular diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD19227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10;
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-611724/70.
                                                       protein variant.
                                                                              in gene therapy. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 4; 266pp;
     280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipases, and lipoprotein diagnosing and treating rdiovascular diseases -
                                                                                             human
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Db Ş đ Ş 밁 Ş B 8 Matches 125 204 185 150 90 71 1,1 77; Conserv X. MLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLTGLAALGL MQDEDGYITLNIXTRKPALV-----SVGPASSFWWRVMALILLILCVGMVVGLVALGI HPTFCENKHYLMCERKAGMTKVDQL ASQSYSBFFYSYWTGLLREDSGKAWLWMDGTFFTSELFHIIDVTSPRSRDCVAILNGMI LYNKAGAHROSPOTEQWKWHGDNCYQFYKDSKSWEDCKYFOLSENSTMLKINKQEDLEFA LKGTFKGHKCSPCDTNWRYYGDSCYGFERHNLTWEESKQYCTDMNATLLKIDNRNIVEYI 149 LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR FSKDCKELKRCVCERRAGMVKPESL KARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED--GKGNMNCAYFHNGKM Conservative -SVMQRNY-----LQDENENRTGTLQQLAKRFCQYVVKQSE 53; Score 352.5; DB 22, Pred. No. 2.3e-27; 3; Mismatches 92; 228 Indels 43; 'n 203 184 124 89 70 6

RASULT 25
AAS11938
ID AAS11
XX
AC AAS11
XX
DT 18-D3
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standard; Protein;

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entry

cardiovascular Human; apolipoprotein;

lipase; e; lipid m

metabolism; lipoprotein protein

n receptor; myocardial

Human lipid metabolism related

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Matches
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Best Local |
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                                                                                                                                                                                                                                                                                             with altered levels of these sequences. All polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them and cells expressing ALLr proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of this polypeptide. Vectors comprising these DNA and protein sequences are also useful for producing ALLr proteins. The nucleic acids and polypeptides of the invention are also useful for the treatment of occlusive cardiovascular diseases, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, coronary artery thrombosis and cerebral artery thrombosis or intracardiac thrombosis and stroke. The nucleotides of the invention are used in gene therapy. The present sequence is human protein related to proteins involved in lipid metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic; coronary artery thrombosis; cerebral artery thrombosis; stroke; intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein receptor polypeptides, useful for preventing diagnosing and treating lipid metabolism disorders, thrombosis and cardiovascular diseases -
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Liu C, Asundi
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22-SEP-2000;
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20-JUN-2000;
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                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                           Local
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DB; AAD19233.
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LKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYI
                                                   LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNTKLAGSLQHVAEKLCR-----E
                                                                                                                        MLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLIGLAALGL
                                                                                                                                                        MQDEDGYITLNIKTRKPALV-----SVGPASSFWWRVMALILLILCVGMVVGLVALGI
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; 2000US-0667298.
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2000US-0598042
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29.1%;
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                                                                                                                                                                                          53;
                                                                                                                                                                                       Score 352.5; DB 22,
Pred. No. 2.3e-27;
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Drmanac
                                                                                  LODENEURTGTLOQLAKRFCQYVVKQSE
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RT, F
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11-APR-2000

25-APR-2000

26-JUN-2000

27-MAY-2000

28-JUN-2000

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14-MAR-2000;
14-MAR-2000;
15-MAR-2000;
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21-MAR-2000;
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02-MAR-2000;
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blood; chondrocyte cell; cell proliferation; cell differentiation;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
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2000US-196000P.
2000US-196187P.
2000US-196690P.
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       2000WO-US20710.
2000US-0644848.
2000WO-US23328.
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2000US-198585P.
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2000WO-US14941.
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2000WO-US13705.
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RESULT 27
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated mucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, catts, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation of differentiation of chondrocyte cells. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 602; 774pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                   Homo sapiens
                                                   Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                  Human
                                                                                                                    06-NOV-2001
                                                                                                                                                     AAM93544;
                                                                                                                                                                                       AAM93544 standard;
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J, Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-602746/68.
DB; AAS46225.
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                                                                                  polypeptide,
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77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLDDDGDTTMSLHSQASATTRHEEPRRTEHRAPSSTWREVALTLLTLCLVLLIGLAALGL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                     LKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVBYI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODEDGYITLNIKTRKEALV-----SVGFASSFWWRVMAJILLILCVGMVVGLVALGI 53
                                                                                                                                                                                                                                                                        FSKDCKELKRCVCERRAGMVKPESI 269
                                                                                                                                                                                                                                                                                                                                                                     KARTH----LIRWVGLSROKSNEVWKWEDGSVISENMFEFLED--GKGNVNCAYFENGKM
                                                                                                                                                                                                                                                                                                        HPTFCSNKHYLMCERKAGMTKVDQL
                                                                                                                                                                                                                                                                                                                                       ASQSYSEFFYSYWTGLLRPDSGXAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMI
                                                                                                                                                                                                                                                                                                                                                                                                          LYNKAGAHROSPOTEQWKWHGDNOYQFYKDSKSWEDCKYFOLSENSTMLKINKQEDLEFA
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                                                                                                                                                                                       Protein;
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atanabe CK, Wood WI,
                                                                                    SEQ ID
                                                                                                                    entry.
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Pred. No. 2.3e-27;
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ang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to primers for synthesising full length cDl clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830 Primers useful for synthesizing use in genetic manipulation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                AAU12400 standard;
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                                                                                                                                                                     245
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su A, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                             MQDEDGYITLNIKTRKPALV------SVGPASSFWWRVMALILLILCVGWVVGLVALGI 53
                                                                                                                                                                                                                                                                                                                                     LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR-----E
                                                                                                                                                                                                                                                                                                        LKGT=KGHKCSPCDTNWRYYGDSCYGFFRHNLTWESSKQYCTDMNATLLKIDNRNIVEYI
                                                                                                                                                                     FSKDCKELKRCVCERRAGMVKPESL
                                                                                                                                                                                                HPTFCENKHYLMCERKAGMTKVDQL
                                                                                                                                                                                                                            ASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMI
                                                                                                                                                                                                                                                     KARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED---GKGNMNCAYFHNGKM
                                                                                                                                                                                                                                                                                 LYNKAGAHROSPOTEQWKWEGDNOYQFYKDSKSWEDCKYFOLSENSTMLKINKQEDLEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                  Protein;
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a T, Nagai
                                                                                                                                                                                                                                                                                                                                                                    -SVMQRNY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 352.5; DB 22;
Pred. No. 2.3e-27;
3; Mismatches 92;
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K, Kojima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
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Human PRO1131 polypeptide sequence

3

24-OCT-2001

(first entry)

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22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
00-MAR-2000;
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01-DEC-1
02-DEC-1
                                                                                    AMU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TWF-alpha) from human blood, the proliferation of differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utrivillar supporting cells or the proliferation of inner ear utrivillar supporting cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secretory and transmembrane; PRO; mammalian; cancer; breast; prostate; cervica; tumour necrosis factor-alpha; T cartilage; ear; proliferation; glucose; free farty acid; sk addpocyte; A-peptide; factor VIIA; gene therapy.
                           monocytes
the PRO po
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
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06-JAN-2000;
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02-DEC-1999,
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30-MAR-2000;
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T-lymphocytes, the release of a cytokine from peripheral blood nocytes (PBMCs), or the proliferation of endothelial cells. Some of PRO polypeptides may modulate glucose or free fatty acid uptake by eletal muscle cells or by adipocytes; or inhibit binding of A-peptides.
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2000WO-US04914.
2000WO-US05004.
2000WO-US05601.
2000WO-US07377.
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2000WO-US15264.
2000WO-US30873.
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2000WO-US08439.
2000WO-US13705.
2000WO-US14042.
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2000WO-US00376.
2000WO-US03565.
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2000WO-US04342.
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Goddard
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99US-0170262.
99WO-US30095.
99WO-US30911.
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99WO-US31243.
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99WO-US28551.
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, Godowski PJ, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe CK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherwood S;
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; TNF-alpha;
skeletal muscle;
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  A-peptide
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17-AUG-1999
17-SEP-1999
15-SEP-1999
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08-OCT-1999
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cell de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynuclectides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSKDCKELKRCVCERRAGMVKPESL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR-----
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                 99WO-US28301.
99WO-US30095.
99WO-US30911.
2000WO-US00276.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
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                                                                                                                                                           99US-0145698.
99US-0146222.
99US-01463396.
99WC-US21090.
99WC-US21547.
99US-0158663.
99WC-US28313.
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99US-0144758.
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99US-0141037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosomal mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry.
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29.1%;
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Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LODENENRIGILOQLAKRFCQYVVKQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:319.
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Porrara N, Fr
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24-FEB-2000;
02-MAR-2000;
15-MAR-2000;
20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                              sequences, and their fragments, can be used as hybridisation probes, i chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagants. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes us in the isolation of human PRO sequences. AAF4407 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO polynucleotides used to produce polypeptides used to bioactive molecules such as toxins, radiolabels or antibospecific cells, to cause targeted cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present in proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF44218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH
                                                                                                                                                                                                                                                                                                                                                                             Sequence
               21-MAR-2001
                                                       AAB50959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes human secreted and transmembrane PRO telns. The PRO proteins have cytostatic activity. The PRO proteins be used for targeted delivery of bloactive molecules, such as ins, radiolabels or antibodies, that cause cell death. PRO nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-032160/04.
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N, Fong S, Gerber H,
i CJ, Gurney AL, Kljav
Stewart TA, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                            MQDEDGYITLNIKTRKPALV-----SVGPASSFWWRVMALILLILCVGMVVGLVALGI 53
                                                                                                                                                      ASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIDVTSPRSRDCVAILNGMI
                                                                                                                                                                                                 LYNKAGAHRCSPCTEQWKWEGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFA
                                                                                                                                                                                                                    LKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDXNATLLKIDNRNIVEYI 149
                                                                                                                                                                                                                                           LFFQYYQLSNTGODTISOMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR-----B
                                                                                                                                                                                                                                                                                         MLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLTGLAALGL
                                                                                                             FSKDCKELKRCVCERRAGMVKPESL
                                                                                                                                                                            KARTH-----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED--GKGNMNCAYFHNGKM
                                                        standard;
                                                                                                                                  HPTFCENKHYLMCERKAGMTKVDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000WO-US04914.
; 2000WO-US05004.
; 2000WO-US05841.
; 2000WO-US06884.
; 2000WO-US07377.
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             (first
                                                         Protein;
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Gerber H, Gerritsen ME, Go
AL, Kljavin IJ, Napier MA
                                                                                                                                                                                                                                                                                                                                              28.0%;
29.1%;
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                                                                                                                                                                                                                                                                                                                                              Score 352.5; DB 22; Pred. No. 2.3e-27;
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Gerritsen ME, Goddard A,
rin IJ, Napier MA, Pan J,
Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                      Mismatches
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MLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLIGLAALGL

-LQDENENRTGTLQQLAKRFCQYVVKQSE

89 70 -SVGPASSFWWRVMALILLILCVGMVVGLVALGI

53

Query Match Best Local S Matches 77

il Similarity 77; Conserv

Conservative

53;

28.0%;

Score 352.5; Pred. No. 2.3; 53; Mismatches

es 92;

Indels Length

43

Gaps

9

BG 22;

280;

MQDEDGYITLNIKTRKPALV-----

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22-UN-1999;
23-UN-1999;
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                                                                                                  The present sequence is one of twenty eight novel PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and histocoelic disorders, and inflammatory, angiogenic and immunological blastocoelic disorders, and inflammatory, angiogenic and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Twenty eight nucleic acids encoding PRO polypeptides for treating various tumors, e.g. breast cancer, and inflammatory, angiogenic and immunological disorders
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Sequence
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AN-2000; 2000WO-US30565.

EB-2000; 2000WO-US3565.

EB-2000; 2000WO-US04341.

EB-2000; 2000WO-US04342.

AR-2000; 2000WO-US05841.

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Watanabe CK,
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                                                                                          The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABQ94682-ABQ65022). The sequences are useful in therapeutic, diagnostic and research methods. The polymuclectities may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, hybridisation probes, primers for PCR, for chromosome and gene mapping, hybridisation probes, primers for PCR, for chromosome and gene mapping, hybridisation probes, primers for PCR, for chromosome and sexpressed for the recombinant production of protein, or in generation of anti-sense NA or RNA. The polymucleotides are useful in diagnostics as expressed sequence tags (ESTs) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungal infection; autoimmune disorder; ccagulation disorder; nootropic;
antiallergic; antiinflammatory; immunosuppressive; neuroprotective;
cytostatic; haemostatic; virucide; antibacterial; fungicide;
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pluripotential state useful for re-engineering damaged or ditissues, transplantation, manufacture of bio-pharmaceuticals development of bio-sensors. The polynucleotides and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity -
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Wehrman T, Drmanac RT;
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central nervous system disease; viral infection;
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             are useful
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          02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
07-SEP-2000;
                                                                               20-JUL-2000;
25-JUL-2000;
25-JUL-2000;
28-JUL-2000;
                                                                                                                                                                                                                                                                                           Human; angiogenesis; PRO atherosclerosis; cardiac
                                                                                                                                                                                                                                                                                                                                        Human
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                                                                                                                                                      09-JUL-2001;
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                                                                                                                                                                                                                                          Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED--GKGNMNCAYFHNGKM
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2000US-219556P.
2000US-220624P.
                                                                                                                                                      2001WO-US21735
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29.1%;
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                                                                                                                                                                                                                                                                                                                                       protein PRO1131 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                           280 AA
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Pred. No. 2.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                gene therapy; endothelial disorder;
hypotensive; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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Query Match
Best Local S
Matches 77
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18-SEP-2000;
24-OCT-2000;
08-NOV-2000;
10-NOV-2000;
21-DEC-2000;
20-DEC-2000;
20-DEC-2000;
22-JAN-2001;
28-FEB-2001;
28-FEB-2001;
28-FEB-2001;
14-MGR-2001;
19-MAR-2001;
10-MAR-2001;
10-MAR-2001;
11-MAY-2001;
10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
30-MAY-2001;
30-MAY-2001;
30-MAY-2001;
30-MAY-2001;
30-MAY-2001;
30-MAY-2001;
30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                             (GODD/)
(GODO/)
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(GURLL/)
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(MARS/)
                                                                                                                                                                                                                                                                                     Baker KP,
Godowski F
                                                                         The present invention provides the protein and coding sequences of hum PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atternosciphy, trauma, cancer, age-related macular degeneration arthriticatherosciphy, trauma, angiogenesis (such as breast carcinoma and liver carcinoma) and wound angiogenesis (such as breast carcinoma and liver carcinoma) and wound
                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                 (STEP/)
(WATA/)
                                                                                                                                                                                          One hundred and eighty seven nucleic acids encoding useful in diagnosis and treatment of cardiovascular infarction), endothelial or anglogenic disorders in
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healing. The
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DB; ABL95643.
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BAKER K P.
FERRARA N.
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
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PAONI N F.
STEPHAN J F.
WATANABE C K
WILLIAMS P M
WOOD W I.
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GERRITSEN M E.
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           Similarity
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PJ, Gurney AL, F
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2000WO-US34956

2001US-0767609

2001US-0796498

2001WO-US06520

2001WO-US06666

2001US-0802706

2001US-0802706

2001US-080283669

2001US-08283669

2001US-08283669

2001US-0828366
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2000WO-US30873.
2000WO-US32678.
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2000US-0665350.
2000US-242922P.
2000US-0709238.
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; 2001WO-US17443.
; 2001WO-US17800.
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; 2001US-0866034.
; 2001WO-US17092.
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2001WO-US00000
   Conservative
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             28.0%;
29.1%;
                                                                   sequence is
                                                                                                                                                                                                                                                                            Gerber H, Gerrit
L, Hillan KJ, Ma
CK, Williams PM,
                                                                                                                                                                        English.
   53
•
              Score 352.5;
Pred. No. 2.3
   Mismatches
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                                                                      PRO
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     Gaps
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RESULT 33
ABB849
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                       23-JUN-2000;

25-JUL-2000;

25-JUL-2000;

25-JUL-2000;

28-JUL-2000;

17-AUG-2000;

17-AUG-2000;

23-AUG-2000;

24-AUG-2000;

18-SEP-2000;

18-SEP-2000;

18-SEP-2000;

18-SEP-2000;

10-NOV-2000;

24-DOCT-2000;

26-DEC-2000;

27-JAN-2001;

28-FEB-2001;

29-MAR-2001;

09-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonis; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast Carcinoma; liver car
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25-MAY-2001;
25-MAY-2001;
30-MAY-2001;
01-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABE88072 to ABE88238 encode the PRO proteins given in ABE84817 to ABE85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular
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L, Hillan KJ, Marsters SA, Pan O
CK, Williams PM, Wood WI, Ye W;
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99WO-US31274.
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98US-081195P 98US-082568P 98US-082568P 98US-082794P 98US-083499P 98US-083499P 98US-083499P 98US-083499P 98US-084414P 98US-084639P 98US-084639P 98US-084639P 98US-085579P 98US-085579P 98US-085582P 98US-085582P 98US-085582P 98US-085700P 98US-086392P 98US-087208P 98US-087208P 98US-08729P 98US-08729P 98US-08729P 98US-08729P 98US-088025P 11 - MAR-1998 11 - MAR-1998 11 - MAR-1998 20 - MAR-1998 20 - MAR-1998 27 - MAR-1998 27 - MAR-1998 31 - MAR-1998 31 - MAR-1998 31 - MAR-1998 01 - APR-1998

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                               ASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMI
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98US-090444P.
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98US-090676P.
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98US-090652P.
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98US-091278P.
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98US-091278P.
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98US-091682P.
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98US-09883P.
98US-09883P.
98US-099754P.
98US-099754P.
98US-099754P.
                                                                                                                                                                                                                                                                                                                                                                    98US-099812P
                                                                                                                                                                                                                                                                                                                  28.0%;
                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                    Score 352.5; DB 24;
Pred. No. 2.3e-27;
3; Mismatches 92;
     228
                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                       280;
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                                                                                                                                                                                                                                                                                                       Gaps
                                                                         203
                                                                                                          184
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                                        244
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15-MAY-1998;
15-MAY-1998;
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16-MAY-1998;
18-MAY-1998;
22-MAY-1998;
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23-JUN-1998;
23-JUN-1998;
23-JUN-1998;
24-JUN-1998;
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98US-087609P 98US-087759P 98US-088025P 98US-088023P 98US-088033P 98US-088031P 98US-088031P 98US-088031P 98US-088031P 98US-088031P 98US-08803P 98US-08803P 98US-08803P 98US-08803P 98US-08803P 98US-08803P 98US-088803P 98US-088803P 98US-088803P 98US-088803P 98US-088803P 98US-08905P 98US-08905P 98US-08905P 98US-089538P 98US-089538P 98US-089538P 98US-089538P 98US-089538P 98US-089538P 98US-089538P 98US-089538P 98US-089538P 98US-089538P

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Вb
16-JAN-2000;
11-FEB-2000;
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20-MAR-2000;
11-MAR-2000;
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08-SEP-1999;
30-NOV-1999;
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02-DEC-1999;
16-DEC-1999;
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C8-MAR-1999;
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2000WO-US03434

2000WO-US04341

2000WO-US05881

2000WO-US05881

2000WO-US06884

2000WO-US14042

2000WO-US14042

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2000WO-US15264

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2000WO-US35522

2000WO-US36666

2001WO-US06520

2001WO-US17809

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2001WO-US21709

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99WO-US28313.
99WO-US28634.
99WO-US28551.
99WO-US30095.
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10-SEP-1998
11-SEP-1998
15-SEP-1998
10-NOV-1998
10-NOV-1998
11-DEC-1998
12-JAN-1999
12-JAN-1999
12-JAN-1999
12-JAN-1999
20-JAN-1999
20-JUL-1999
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20-JUL-1999
11-APR-1999
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11-APR-1999
11-OCT-1999
09-SEP-1999
10-NOV-1999
10-NOV-1999
10-JUN-2001
10-JUN-2001
10-JUN-2001
10-JUN-2001
10-JUN-2001
10-AUG-2001
11-AUG-2001
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17-AUG-1998;
17-AUG-1998;
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11-JUN-1998;
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2000US-187202P.
28UUS-180997.
98US-0218517.
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99US-0380138.
99US-0380138.
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99US-0423741

290US-079238

2001US-0802706

2001US-0866034

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2001US-082636

2001US-0926419

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99US-131294P.
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98US-096891P.
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                                                                                                                                                                                                   Henzel
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Baker KP, Gu Goddard , Smith <, Ъ Gurney AL, Watanabe CK, Hebert C, Wood Σ¦Ω, Kabakoff 보 ()

N-ESDB; 2003-328851/31. ACA57998.

Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful treating tumor, preferably cancer, or for treating neuronal, glial, hypothalamic, stromal, inflammatory, angiogenic and immunologic treating tumor, prefer hypothalamic, stromal, disorders for

Claim 32; Fig 18; 186pp; English

The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its associated signal peptide or PRO polypeptide extracellular domain with or without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, gastric, pancreatic, vulval, thyroid, central nervous system cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its agonists. The PRO polypeptide or an antibody binding to it is useful in the preparation of a medicament for treating a condition which is

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Best Local
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16-SEP-1998;
07-OCT-1998;
01-DEC-1999;
18-MAX-1999;
14-MAX-1999;
02-UUN-1999;
01-SEP-1999;
01-DEC-1999;
01-DEC-1999;
01-DEC-1999;
02-DEC-1999;
03-DEC-1999;
05-DAX-2000;
18-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; TNF-alpha release, arthritis; tumour necrosis factor alpha; chondrocyte cell; bone disorder cartilage disorder; sports inimmy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU65869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYNKAGAHROSPOTEQWKWHGDNOYQFYKDSKSWEDOKYFOLSENSTYLKINKQEDLEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; transmembrane protein;
 2000WO-
2000WO-
2000WO-
                                                                                                                                                                                                                                                                               2002US-0188767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
 98WO-US1330
98WO-US21141
98WO-US2108
99WO-US10733
99WO-US10733
99WO-US20111
99WO-US20111
99WO-US21090
99WO-US21090
99WO-US21090
99WO-US28551
1000WO-US04341
2000WO-US043442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 352.5; DB 24;
Pred. No. 2.3e-27;
3; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID 602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LODENENRIGILOQLAKRECOYVVKOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung tumour;
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         15-MAR-2000;
17-MAY-2000;
17-MAY-2000;
22-MAY-2000;
24-AUG-2000;
28-JUN-2000;
20-DEC-2000;
20-DEC-2000;
21-DEC-2000;
21-DEC-2000;
22-JUN-2001;
20-JUN-2001;
20-JU
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24-FEB-2000;
01-MAR-2000;
02-MAR-2000;
     11-MAR-1998;
11-MAR-1998;
20-MAR-1998;
20-MAR-1998;
27-MAR-1998;
31-MAR-1998;
31-MAR-1998;
31-MAR-1998;
01-APR-1998;
01-APR-1998;
01-APR-1998;
01-APR-1998;
01-APR-1998;
01-APR-1998;
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02-APR-1998;
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22-APR-1998;
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29-APR-1998;
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2000WO-US05004.
2000WO-US05601.
2000WO-US05841.
2000WO-US06884.
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; 2001WO-US21735.
; 2001WO-US27099.
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2000WO-US34956.
2001WO-US06520.
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2000WO-US13705
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2001WO-US19692
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2000WO-US30952
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2000WO-US20710
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2000WO-US14941.
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97US-066375P
97US-069375P
97US-069425P
97US-069870P
97US-068017P
97US-068017P
98US-077450P
98US-077649P
98US-0778886P
98US-078886P
98US-079664P
98US-0797868P
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9708-063121P.
9708-063121P.
9708-063541P.
9708-063544P.
9708-063564P.
9708-063764P.
9708-063870P.
9708-064103P.
9708-064103P.
9708-066311P.
9708-0664103P.
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98US-080127P.
98US-080127P.
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98US-081195P.
98US-081195P.
98US-0811888P.
98US-0812589P.
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98US-08379PP.
98US-08349PP.
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98US-08349PP.
98US-08349PP.
98US-084414P.
98US-08464PP.
98US-08464PP.
98US-08464PP.
98US-084659P.
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97US-062250P.
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15-MAY-1998 18-MAY-1998 18-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 22-MAY-1998 23-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 25-JUN-1998 25-JU

98US-085582P 98US-086023P 98US-086392P 98US-086392P 98US-087098P 98US-087709P 98US-087759P 98US-088782P 98US-088028P 98US-088028P 98US-088029P 98US-088029P 98US-088029P 98US-088028P 98US-0880212P 98US-088212P 98US-0888762P 98US-0888762P 98US-0888762P

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RESULT 37
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Best Loc
Matches
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18-AUG-1998;
18-AUG-1998;
26-AUG-1998;
26-SEP-1998;
07-SEP-1998;
09-SEP-1998;
09-SEP-1998;
16-SEP-1998;
07-OCT-1998;
01-DEC-1998;
08-MAR-1999;
14-MAY-1999;
02-JUN-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; transmembrane protein; cytostatic; gene Therapy; TNF-Agonist-Alpha; chondrocyte stimu_ator; transmembrane therapy; TNF-Agonist-Alpha; chondrocyte stimu_ator; tradecral tumour; Inug tumour; con tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFFQYYQLSNTGQDTISQMEERLGNTSCELQSLQVQNIKLAGSLQHVAEKLCR-----E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
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llarity 29.1%;
Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted and
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98US-096559P-
98US-096559P-
98US-097022P-
98US-097955P-
98US-097971P-
98US-097971P-
98US-098714P-
98US-098713P-
98US-0988718P-
98US-098803P-
98US-098821P-
98US-098821P-
98US-098821P-
98US-098821P-
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98US-098821P-
98US-098821P-
98WO-US19330.
98WO-US25108.
98WO-US25108.
99WO-US05528.
99WO-US10733.
99WO-US12752.
99WO-US20111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
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Pred. No. 2.3e
53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280
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                                                                                                                                                                                                                                                                                                                                               cervical tumour; liver tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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2.3e-27;
2.92;
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22-JUN-1998; 22-JUN-1998; 22-JUN-1998;

3-090246P. 3-090252P. 3-090254P. 3-090429P. 3-090435P. 3-090444P.

3-090461P. 3-090535P. 3-090540P. 3-090676P. 3-090678P.

-090690P

17-JUN-1998 18-JUN-1998 19-JUN-1998

-089908F.

11-JUN-1998; 11-JUN-1998; 12-JUN-1998; 12-JUN-1998; 12-JUN-1998; 16-JUN-1998; 17-JUN-1998; 17-JUN-1998;

98US-089090P. 98US-089105P. 98US-089514P. 98US-089514P. 98US-089538P. 98US-089538P. 98US-089538P. 10-JUN-1998;

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22-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 26-JUN-1998 26-JUN

3-090694 p.
-090696 p.
-090696 p.
-0910100 p.
-091148 p.
-091622 p.
-091622 p.
-091622 p.
-09466 p.
-09598 p.
-096766 p.
-096766 p.

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-096891P

\$20.86 \$2

22-APR-1998; 22-APR-1998; 28-APR-1998; 29-APR-1998; 29-APR-1998;	-APR-1998; -APR-1998; -APR-1998;	-APR-1998; -APR-1998; -APR-1998; -APR-1998;	MAR-1998; APR-1998;	MAR-1998; MAR-1998;	MAR-1998; MAR-1998;	MAR-1998; MAR-1998;	DEC-1997; MAR-1998;	DEC-1997;	NOV-1997; DEC-1997;	NOV-1997; NOV-1997;	OCT-1997; NOV-1997;	OCT-1997; OCT-1997;	OCT-1997; OCT-1997;	OCT-1997;	OCT-1997; OCT-1997;	SEP-1997; OCT-1997;	AUG-2001; 20	TUN-2001; 20	JUN-2001; 20	DEC-2000; 20	VOV-2000; 20	TUN-2000; 20	AY-2000; 20	AY-2000; 20	AR-2000; 20	IAR-2000; 20 IAR-2000; 20	EB-2000; 20	EB-2000; 20	AN-2000; 20	EC-1999;	
8; 98US-082/04F. 8; 98US-082797P. 8; 98US-083322P. 8; 98US-083495P. 8; 98US-083495P.	98US-081838P. 98US-082568P. 98US-082569P.	9805-080332P. 9805-081049P. 9805-081070P. 9805-081195P.	98US-080194P. 98US-080327P.	98US-0/9664F. 98US-079786F. 98US-0801075	98US-078886P. 98US-078939P.	98US-077632P. 98US-077649P.	97US-068017P. 98US-077450P.	97US-069425P. 97US-069870P.	97US-06677ZP. 97US-069335P.	97US-066120P. 97US-066466P.	97US-064103P. 97US-065311P.	97US-063734P. 97US-063870P.	97US-063544P. 97US-063564P.	97US-063540P. 97US-063541P.	97US-063120P. 97US-063120P. 97US-063121P.	97US-059266E. 97US-062250E.	97US-059263P.	01WO-US21066.	01WO-US17800.	00WO-US34956.	00W0-US23328. 00W0-US30952.	00WO-US15264. 00WO-US20710.	00WO-US14941.	00WO-US13705.	00WO-US06884. 00WO-US08439.	00WO-US05601. 00WO-US05841.	00WO-0304414.	00WO-US04342.	00WO-US00219. 00WC-US04341.	99WO-US28551. 99WO-US31274.	9WO-US2830
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                                                                                                                                                      PRO polypeptide; secreted and transmembrane protein; necrosis factor-alpha; TNF-alpha; blood; proliferation; entiation; chondrocyte; tumour; genetic disorder;
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l Similarity 29.1%;
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The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The CR properties are useful for detecting other PRO polypeptides, for general proteins. The PRO CC polypeptides are useful for detecting other PRO polypeptides, for CC polypeptides, and for for identifying agonists or antagonists. CC polypeptides, and for for identifying agonists or antagonists. CC polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of chondrocytes, and detecting the propertides are useful as hybridisation probes, in chromosome and CC gene mapping, in the generation of antisense RNA and DNA, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green mapping, in the generation of antisense RNA and DNA, in the green the application of antisense RNA and DNA, in the green the application of antisense RNA and DNA, in the green through the discorders, and in gene therapy. ABU66870-ABU66844 represent the human green contraction of the invention.
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09-JUL-2001;
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06-AUG-2001;
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Smith V, Stewart TA,
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                                                                                                                      Seguence
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1 MQDEDGYITLNIKTRKPALV-----SVGPASSFWWRVMALILLLLLCVGMVVGLVALGI
                                                                      Similarity
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29.1%;
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N, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                   53;
                                                     Score 352.5; I
Pred. No. 2.3e
53; Mismatches
                                                      5; DB 24;
2.3e-27;
nes 92;
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14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
29-OCT-1998;
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12-JUN-1998;
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08-NOV-2000;
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09-JUL-2001;
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01-MAR-2001;
25-MAY-2001;
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28-JUL-2000;
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23-AUG-2000;
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21-MAR-2000;
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18-FEB-2000;
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7-MAY-2000;
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2000WO-US07377.
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2003-331925/31.
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wart TA,
                            1 A, Godow
Tumas D,
                                       Godowski PJ,
                              Watamabe CK,
                             Gurney AL, She
                             Sherwood S;
WI, Zhang Z;
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New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer -

458; 659pp;

CC of detecting PRO proteins, methods for stimulating the release of CC (INF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the CC (and the proliferation of differentiation of chondrocyte cells, the release or CC proteoglycans from cartilage, proliferation of finner ear urticular proteoglycans from cartilage, proliferation of finner ear urticular cc supporting cells, the proliferation of T-lymphocyte cells, the release of continuous from peripheral blood mononuclear cells (PBMC), or the continuous from peripheral blood mononuclear cells (PBMC), or the continuous from peripheral blood mononuclear cells (PBMC), or the continuous from peripheral blood mononuclear cells (PBMC), or the continuous from the binding of A-peptide to factor VIIA, cor or the differentiation of adipocyte cells, a method for detecting the coresence of a tumour in a mammal and an oligonucleotide probe derived coresence of a the nucleotide sequences cited above. The nucleic acids and colypeptides are useful for treating inflammatory diseases, organ cartillar, atherosclerosis, cardiae injury, infertility, birth defects, organic failure, atherosclerosis, cardiae injury, infertility, birth defects, organic failure, atherosclerosis, cardiae injury, infertility, birth defects, organic failure, atherosche and gene mapping, and in generating antisense RNA cor DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. at least 80% identical to, or the full-length coding sequence of, any of the 275 nuclectide sequences, encoding the corresponding PRO polyceptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor 'le') 280

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245 FSKDCKELKRCVCERRAGNVKPESL 269	204 HPTFÇENKHYLMÇERKAĞMTKVDQL 228	185 ASQSYSEFFYSYWTGLLRPDSGKAMLWMDGTPFTSELFHIIDVTSPRSRDCVAILNGMI 244	150 KARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNNNCAYFHNGKM 203	125 LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFA 184	90 LKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWESSKQYCTDMNATLLKIDNRNIVEYI 149	71 LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQVVAEKLCR 124	54 WSVMQRNYLQDENENTGTLQQJAKRFCQYVVKQSE 89	11 MLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLIGLAALGL 70	1 MQDEDGYITLNIKTRXPALVSVGPASSEWWRVMALILLILCVGMVVGLVALGI 53	Similarity 7; Conservat	76 DB 24: Length 280:

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28-PEB-2001;

01-JUN-2001;

20-JUN-2001;

29-JUN-2001;

29-JUN-2001;

29-JUN-2001;

26-JUN-1998;

07-OCT-1998;

07-OCT-1998;

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07-DEC-1999;

14-MAY-1999;

14-MAY-1999;

14-MAY-1999;

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14-MAY-1999;

15-AUG-1999;

25-AUG-1999;

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01-MAR-2000;
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24-AUG-2000;
08-NOV-2000;
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2000WO-US114042
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2000WO-US1264
2000WO-US23710
2000WO-US23328
2000WO-US23328
2000WO-US2952
2000WO-US2952
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2001WO-US1956
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2000WO-US04414.
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factor alpha; chondrocyte cell; tumour; gene therapy;
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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that Specifically binds to the PRO polypeptide, a method for stimulating the contacting the blood a PRO polypeptide, a method for stimulating the CC contacting the blood a PRO polypeptide, a method for stimulating the CC contacting the blood a PRO polypeptide, a method for stimulating the CC contacting the blood a PRO polypeptide, a method for stimulating the CC cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonuclectide probe derived from any of the PRO nuclectide sequences. The nuclectide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in CC e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for CC chromosome dentification, as chromosome markers, as therapeutic agents, for stimulating the release of TNP-alpha from human blood, for a stimulating the presence of a tumour. The PRO polypeptides and security calls the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ABU67406-ABU67710 are the PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2001;
10-MAY-2001;
25-MAY-2001;
05-JUN-2001;
05-JUN-2001;
18-JUL-2001;
30-JUL-2001;
13-AUG-2001;
13-AUG-2001;
16-AUG-2001;
16-AUG-2001;
28-AUG-2001;
04-SEP-2001;
15-JAN-2002;
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Pan J,
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N-PSDB; ACA06000.
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2001US-0918585.
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2001US-0929404.
2001US-0931836.
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2001US-0854280.
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stanabe CK, Wood WI,
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77; Conserv
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                         HPTFCENKHYLMCERKAGMTKVDQL
                                                                            KARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED--GKGNMNCAYFHNGKM
                                                                                                       LYNKAGAHRÓSÞÓTEQWKWHGDNÓYQFYKDSKSWEDCKYFÓLSENSTMLKINKQEDLEFA
                                                                                                                                                         LFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCR----E
FSKDCKELKRCVCBRRAGMVKPESL
                                                   ASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMI
                                                                                                                                 LKGTFKCHKCSPCDTNWRYYGDSCYGFFRHNLTWEBSKQYCTDMNATLLKIDNRNIVEYI
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Pred. No. 2.3e-27;
i3; Mismatches 92;
 269
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Gaps

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05-GCT-1999
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07-DE
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01-DEC-1998;
05-JAN-1999;
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12-JUN-1998;
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99WO-US21090.
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                                                       Novel isolated PRO po
and PRO1375, which st
are therapeutically treatments
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N-PSDB; ABX89369.
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D-US04342.
D-US04414.
D-US04914.
                                                                      polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 stimulate proliferation of stimulated T-lymphocytes y useful for enhancing immune response and in cancer
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                                                                                                                                                                                            Deforge L, Desnoyers L,
A, Godowski PJ, Gurney.
Tumas D, Watanabe CK, W
                                                                                                                                                                                              L, Filvaroff E, Gay AL, Sherwood S; Wood WI, Zhang Z;
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CC The invention describes an isolated human PRO polypeptide. The PRO CC polypeptides are useful in detecting PRO polypeptides in a sample, in a coll inhing a bloactive molecule to a cell expressing a FRO polypeptide, and CC in modulating at least one biological activity of a cell expressing a PRO CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus constitute adrenal corrical capillary endothelial provent, and PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO136, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137, PRO137,
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                                                          Human, PRO; cytostatic; chromosome mapping; gene mapping; protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte differentiation; chondrocyte proliferation; tumour.
                   Homo sapiens
                                                        protein electrophoresis; tum
chondrocyte differentiation;
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(GETH) GENENTECH INC.

Grimaldi Roy MA, Zhang Z; Zhang Ferrara Ashkenazi z i AJ, Baker KP, Botstein D, Desnoyers L, Eaton N, Fong S, Gerber H, Gerritsen ME, Goddard A, JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Stewart TA, Tumas D, Watanabe CK, Williams PM, Godowski Paoni NF; Wood WI; DL; ₽J;

WPI; 2003-247083/24. N-PSDB; ABX80325.

Novel isolated PRO polypeptides e.g., PRO826, PRO1368, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

Claim 12; Fig 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bloactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO186 or PRO535, PRO926, PRO8187 induce c-fos in endothelial capillar, and endothelial capillar and prossing prossing a prossing or treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1346, PRO1346 and PRO1375 stimulate proliferation of
05-NOV-1997;
16-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813, PRO813 and PRO11666 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
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Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound leartification of the provider; cancer; tumour; immune response adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinits pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte prolife
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98US-097621P.
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98US-098054P.
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Pred. No. 2.3e-27;
3; Mismatches 92;
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          disease; chondrocyte proliferation;
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2001US-0990562. 97WO-US20069. 98WO-US19437. 98WO-US1141. 98WO-US21141. 98WO-US21141. 98WO-US21147. 99WO-US21147. 99WO-US21147. 99WO-US21547. 99WO-US21547. 99WO-US21647. 99WO-US21647. 99WO-US28631. 99WO-US2665. 2000WO-US04341. 2000WO-US04341. 2000WO-US05684. 2000WO-US05684. 2000WO-US05684. 2000WO-US1376. 2000WO-US1376. 2000WO-US1376. 2000WO-US13358. 2000WO-US13358. 2000WO-US13358. 2000WO-US13358. 2000WO-US22331. 2000WO-US23527.	redifferentiation; sp
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17-AUG-1998
                  Human secreted/transmembrane protein,
                                                      01-MAY-2003 (first entry)
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                                                                                                                            standard;
                                                                                                                                                                                                                                                                                         ASQSYSEFFYSYMTGLLRPDSGKAMLWMDGTPFTSELFHIIDVTSPRSRDCVAILNGMI
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98US-095318P

98US-095325P

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98US-096143P

98US-096143P

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29.1%;
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                                                                                                                            280
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Pred. No. 2.3e-27;
3; Mismatches 92;
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15-SEP-1999

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10-MAR-2000

10-MAR-2000

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pharmaceutical; diagnostic; therapeutic; gene therapy.
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2000WO-US04344
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The invention discloses isolated PRO secreted/transmembrane polypeptides CC comprising a sequence without signal peptide and the nucleic acid CC encoding them. The polypeptides can be used to raise antibodies that Specifically bind to the PRO polypeptide, for linking a bioactive CC molecule to a cell expressing a PRO protein and for modulating at least CC one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful in gene therapy, in chromosome CC identification, as chromosome markers, or in generating probes. The PRO CC polypeptides are useful as molecular markers for protein CC polypeptides are useful as molecular markers for protein CC recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful CC in diagnostic assays for PRO, and in affinity purification of PRO from CC recombinant cell culture or natural sources. The sequences presented in CC ABUGOT8-ABUGOZ4 are the PRO polynucleotides of the invention.

CC Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html.
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Roy MA, Stewart TA,
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                                                    Sequence
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Gerber H, Gerritsen ME, Goddard A,
AL, Kljavin IJ, Napier MA, Pan J,
Tumas D, Watanabe CK, Williams PM,
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Score 352.5; DB 24;
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Pred. No. 2.3e-27;
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07-OCT-1996
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53; Mismatches
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08-MAR-1999

02-UNN-1999

15-SEP-1999

30-NEC-1999

31-DEC-1999

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                                                                                                                                                                                                                        Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer; Lung cancer; breast cancer;cancer; gene therapy.
                                                                                                                                        19-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                    standard;
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comprising a sequence without signal peptide and the nucleic acid cencoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive conclude to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymucleotides are also useful as pharmaceuticals, diagnostics, come biological activity of a cell. The PRO polypeptides or polymucleotides are also useful as pharmaceuticals, diagnostics, come biological activity of a cell. The PRO polypeptides or commandiate and protein and for modulating at least concerns and commandiate are so incompared to the concerns and diagnostic determination cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as compared to the compared to the concern as the protein and colon, lung or breast cancers. The propagation of the presence of these cancers or for chromosome identification. The PRO genes concerns the protein as hybridisation probes or for screening libraries of human colon, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences or presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.
Query Match
Best Local S
Matches 77
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17-JUN-1998;
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28-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                           invention discloses
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98US-089801P.
98US-089907P.
98US-089908P.
2001US-0941992.
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                28.0%;
                                                                                                                                                                                                                                                                                                                                                                                             isolated PRO secreted/transmembrane polypeptides ithout signal peptide and the nucleic acid peptides can be used to raise antibodies that
              Score 352.5; DB 2
Pred. No. 2.3e-27;
                               24;
                               Length
                                                                                                             of the invention
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Godowski PJ;
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Conservative

53;

Mismatches

92;

Indels

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RESULT 50 ABU56236 ID ABU56

ABU56236 standard; Protein; 280 AA

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99WO-US23089

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                                                                                                                                                                                                                                                                                                                      hepatic lectin 2 - natural killer cel asialoglycoprotein MK-cell receptor p mast cell function lectin-like oxidiz hepatic lectin-c natural killer cel gene 17.5 protein hom LY-49F-GZ antigen natural killer cel HIV gpl20-binding natural killer cel
                                    lectin M-ASGP-BP p
hNKR-Pla protein -
Ly-49D-GE antigen
natural killer cel
Ly49c - mouse
lectin, galactose/
natural killer cei
T-cell surface gly
natural killer cel
Ly49z-GE antigen
asialoglycoprotein
IGE Fc receptor, 1
                  IgE Fc receptor, 1
NKR-P1 protein hom
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ALIGNMENTS

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N;Ālternate names: asialoglycoprotein receptor RHL-2/3 (ASG2-R2/3) (;Species: Rattus norvegicus (Norway rat) (;Species: Rattus norvegicus (Norway rat) (;Date: 31-Mar-1988 #sequence revision 09-Apr-1998 #text_change 22-Jun-1999 (;Accession: B28402; A28462; Ā31601; A26888; A25417 R;Halberg, D.F.; Wager, R.E.; Farrell, D.C.; Hildreth IV, J.; Quesenberry, M.S.; Loeb, J. Biol. Chem. 262, 9828-9838, 1987 J. Biol. Chem. 262, 9828-9838, 1987 A;Title: Major and minor forms of the rat liver asialoglycoprotein receptor are independence number: A28462; MUID:87250656; PMID:3597443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 201-259,'C',261-281,'ND',284-301 <DRI>C);Comment: Calcium is required for ligand binding. C;Superfamily: hepatic lectin; C-type lectin homology C;Keywords: endocytosis; glycoprotein; lectin; liver; F;2-60/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-152,'A',154-201,'I',203-259,'C',261-301 <MCP>
A;Cross-references: GB:M16347; NID:g206648; FIDN:AAA42038.1; PID:g206649
A;Note: the authors translated the codon GCA for residue 153 as Arg and ATT for resi
R;Drickamer, K.; Mamon, J.F.; Blins, G.; Leung, J.O.
J. Biol. Chem. 259, 770-778, 1844
A;Title: Primary structure of the rat liver asialoglycoprotein receptor: structural
A;Reference number: A25417; MUID:84111554; PMID:6319386
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A;Residues: 88-96,'X',98-118,'X',120;129-158;177-182,'X',184,'X',186-189;192-290,'C'
R;Sanford, J.P.; Elliott, R.W.; Doyle, D.
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Mol. Cell. Biol. 7, 1841-1847, 1987
Mol. Cell. Biol. 7, 1841-1847, 1987
A;Title: Identification and characterization of cDNA clones encoding A;Reference number: A26888; MUID:87257885; PMID:3600647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Asialoglycoprotein receptor genes A; Reference number: A31601; MUID:89170119;
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DQYCQMENAHLLVINSREEQEFVVXHRGAFHIWIGLTDKDGS--WKWVDGTEYRSNFKNW 252
                                                                                                                  DHSTLLFHLKHFPLDLRTLTCQLAFFLSNGTEC---CPVNWVEFGGSCYWFSRDGLTWAEA 194
                                                                                                                                                                                                                                                                                               I----WSVMQR--
                                                 KQYCTDMNATLLKIDNRNIVBY-IKARTHLIRWVGLSRQKSNBVWKWBDGSVISENM---
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24.9%;
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Pred. No. 1.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                         -NYLQDENENRIGILQQLAKRECQYVVKQSELKG 92
                                                                                                                                                                       -KGHKCSPCDTNWRYYGDSCYGFFRHNLTWBES 126
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 \ensuremath{\mathsf{PMID}}\xspace:3234178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 301
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RESULT
S13165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related A;Reference number: PT0372; MUID:91178434; PMID:2007850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C/Accession: PTC375, S15671, S19110
                                                                                                                                                                                                                                            A;Cross-references: EMBL:X53042; NID:g53104; PIDN:CAA37211.1; C;Superfamily: hepatic lectin; C-type lectin homology C;Keywords: glycoprotein; liver; transmembrane protein F;170-293/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                          R;Sanford, J.P.; Doyle, D.
Biochim. Biophys. Acta 1087, 259-261, 1990
A;Title: Mouse asialoglycoprotein receptor
A;Reference number: S13165; MJID:91027942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asialoglycoprotein receptor - mous N_7Alternate names: hepatic lectin
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A; Residues: 1-216 < HOU>
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A; Residues: 1-301 <SAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 CYKNNCYQFFDESKNWYESQASCMSQNASLLKVYSKEDQDLLKLVKS----YHWMGLVHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 AFTQPDNWQGHEEG-GSEDCAEILSDGLWNDNFCQQVNRWACERKRDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                       141 DNRNIVEY-IKARTHLIRWVGLSRQKSNEVWKWEDGSVISENM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 LVALGEWSVMQRNYLQDENENRIGILQQLAKRFCQYVVKQSELKGIFKGHKCSPCDTNWR
                                                                                                                                                                 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYGDSCYGFFRHNLTWEESKQYCTDMNATLLKI---DNRNIVEYIKARTHLIRWYGLSRQ
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  NSREEQDFVVKHRSQFHIWIGLTDRDGS--WKWVDGTDYRSNYRNWAFTQPDNWQGHEQG
                                                                                                                        COYVVKOSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTNGSWQWEDGSILSPNLLTIIEMQKG--DCALYASSFKGYIENCSTPNTYICMQR
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31.2%;
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Pred. No. 1.4e-11;
5; Mismatches 57
                                                                                                                                                                                                         Score 200.5;
                                                                                                                                                                                       Pred.
                                                                                   CPVNWVEFGGSCYWFSRDGLTWAEADQYCQLENAHLLVI
                                                                                                                                                                 Mismatches
                                                                                                                                                                                       No.
                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequence:
PMID:2223888
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                                           189
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Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A;Title: A secretion inhibitory signal transduction mole A;Reference number: I59421; MUID:98016176; PMID:7568140
A;Accession: I59421
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I59421
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A;Residues: 1-223 <GIO>
A;Residues: 1-223 <GIO>
A;Cross-references: GB:M62891; NID:g205722; PIDN:AAA41710.1; PID:g205723
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: transmembrane protein
F;94-210/Domain: C-type lectin homology <LCH>
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A35917
NK-cell receptor P1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Apr-1991 #sequence_revision 12
C;Accession: A35917
                                                                                                                                                                                  A;Gene: mafa
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Science 249, 1298-1300, 1990
                                                                                                                                                                                                                                              A; Molecule type: mRNA
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A;Accession: A35917
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                                                                                                                                                                                                                                                             ;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                         ast cell function associated antigen -;Species: Rattus norvegicus (Norway rat
                                                                                                                      Matches
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                                                                                                                                  Similarity
 YIQDENENRIGTIQQLAKRFCQYVVKQSELKGTFXGHKCSFCDTNWRYYGDSCYGFFRHN 120
                                                MADNSIYSTLEL----PAAPRVQDDSR--WKVKA-VLHRPCVSYLV-MVALGLLTVILMS
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                                                                              MQDEDGYITLNIKTRKPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENWKWINGSTLNSDVLSITGDTEKD-SCASVSQDKVLSESCDSDNIWVCQKE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIR---WVGLSRQKS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYLSIKPSKTAAGAQCVSPPSIPPDACRCPRSHRIAIKISCAGLIIIIVLAIVGKSIIVRV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLNIKTRKPAL------VSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRN 60
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                                                                                                                    Conservative
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                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
                                                                                                               Score 175.5; DB 2;
Pred. No. 2.1e-08;
2; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 187; DB 2;
Pred. No. 2.3e-09;
0; Mismatches 84
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on 02-Jul-1996
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                                                                                                                                                                                                           PIDN:CAA56208.1;
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type: DNA
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A;Cross-references: GB:J03188; NID:g212246; PIDN:AAAA3937.1; R;Bezouska, K.; Crichlow, G.V.; Rose, J.M.; Taylor, M.E.; Dri J. Biol. Chem. 266, 11604-11609, 1991
A;Title: Evolutionary conservation of intron position in a su A;Reference number: A40427; MUID:91268022; PMID:2050668
A;Accession: A40427
                                                                                                                                                                                                                    A;Note: some or all of the cysteines are involved in disulfide bonds A;Note: residues 24-48 form an uncharged, hydrophobic region that may R;Mellow, T.E.; Halberg, D.; Drickamer, K.
J. Biol. Chem. 263, 5468-5473, 1988
A;Title: Endocytosis of N-acetylglucosamine-containing glycoproteins A;Reference number: A28194; MUID:88186849; PMID:3281941
                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 256, 5827-5839, 1981
A; Title: Complete amino acid sequence of a A; Reference number: A03167; MUID:81215504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Gallus gallus (chicken)
C;Date: 08-Oct-1981 #sequence_revision
C;Accession: A03167; A28194; A40427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: LDX-1
C;Species: Mis miner:
                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-207 < MEL>
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-207 < DRI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 245, 841-846, 1998
A;Title: High affinity binding of oxidized LDL to mouse
A;Reference number: JE0111; MUID:98249801; PMID:9588202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JE0111
R;Hoshikawa, H.; Sawamura, T.; Kakutani, M.; Aoyama, T.; Nakamura, T.; Masaki,
                                                                                                                                                                                                     A; Accession: A28194
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A03167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-363 < HOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JE0111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 22-May-1998 #sequence_revision 29-May-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 SWEKNROTCOSLGGOLLQINGADDLTFILQAISHTTSPFWIGLHRKKPGOPWLWENGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWEESKQYCTDMNATLLKIDNRNIVEYI-KARTHLIR--WVGLSRQXSNEVWKWEDGSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLQKNQNLQEALQRAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENMFEFLEDGKGNM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLYQRTLCCGS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.9%; Sc
24.9%; Pr
ative 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 175; DB 2; LC.
Pred. No. 4.8e-08;
Pred. Cohes 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane receptor PMID:7240175
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ickamer, K.
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N;Contains: natural killer cert.
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_char
C;Accession: PT0372; PT0373
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a family of related
%.Peference number: PT0372; MUID:91178434; PMID:2007850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 15/1; 50/1; 75/1; 125/3; 163/2
()Superfamily: hepatic lectin; C-type lectin; lectin; transmembrane protein
F;1-23/Domain: intracellular #status predicted <INT>
F;24-47/Domain: transmembrane #status predicted <EXT>
F;48-201/Domain: extracellular #status predicted <EXT>
F;78-201/Domain: extracellular #status predicted <EXT>
F;78-201/Domain: extracellular momology <LCH>
F;1/Modified site: acetylated amino end (Met) #status experimental
F;67/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C;Ge
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A;Cross-references: GB:M63
C;Comment: Hepatic lectin
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                                                                                                                                                                       F;119-229/Domain: C-type lectin homology <LCH>
F;102,103,151,180/Binding site: carbohydrate (Asn) (covalent)
F;109-130,147-229,208-221/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                             C/Superfamily: natural killer cell receptor P1; C-type C/Keywords: alternative splicing; glycoprotein; transf F;71-98/Domain: transmembrane #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:X54868;
A;Experimental source: natural
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    natural killer cell receptor group 2, splice form A - human N,Alternate names: NKG2-A, NKG2-B N,Contains: natural killer cell receptor group 2, splice form
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                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:KLRC1; NKG2
A;Cross-references: GDB:138773; OMIM:161555
A;Map position: 12pter-12qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-95,114-233 < HOU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X54867; NID:g35056; PIDN:CAA38649.1; A;Experimental source: natural killer cell
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A; Residues: 1-233 < HOU1>
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Best Local S
Matches 41
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;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
;Accession: PT0372; PT0373
                                                                                              Matches
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                                                                                                              Similarity
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                                        ILLILCVGMVVGLVALGIMSVMQRNYLQDBNENRTGTLQQLAKRFCQYVVKQSELKGTFK
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ILGIICLILMASVVTI---VVIPSTLIQRHNNSSLNTRTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WKEGEPNNRGFNEDCAHVWTSGQWNDVYCTYECYYVCEK 203
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killer cell
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                                                                                           28;
                                                                                       Score 174; DB 2;
Pred. No. 3.6e-08;
8; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 174.5; DB 1 Pred. No. 2.9e-08;
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Local

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Mismatches

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Indels

49;

Gaps

10;

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A;Cross-references: GB:M77677; NID:g200060; PIDN:AAA39823.1; PID:g200061 A;Experimental source: NK cells, C57BL7B A;Note: sequence extracted from NCBI backbone (NCBIN:52380, NCBIP:52381) C;Superfamily: natural killer cell receptor P1; C-type lectin homology C;Keywords: transmembrane protein F;94-210/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA, A; Residues: 1-257 <BER > A; Residues: 1-257 <BER > A; Cross-references: GB: M88072; NID:g505324; PIDN:AAA48558.1; C; Superfamily: C-type lectin homology F;129-241/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                     J. Immunol. 147, 1701-1708, 1991
A; Title: A family of genes selectively coexpressed in a A; Reference number: A46467; MUID:91349596; PMID:1880421
                                                                                                                                                                                                                                                                                                                                            NKR-P1 protein homolog - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Bernot, A.; Zoorob,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene 17.5 protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
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                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-223 < GIO>
                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                    A; Accession: B46467
                                                                                                                                                                                                                                                                                                             C;Accession: 346467
R;Giorda, R.; Trucco, M.
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A; Title: Linkage of a new member of the
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                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSPREPFSHVCPNAWVGFQGKCYYFSDTESDWNSSREHCHRLGASLATLDTKEBMEFMLQ 178
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Score 170.5;
Pred. No. 7.1
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Pred. No. 4.5e-08;
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                Length 223;
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C;Accession: PT0374
R;Houchins, J.P.; Yabe, T.; McSherry, C.; B
J. Exp. Med. 173, 1017-1020, 1991
A;Title: DNA sequence analysis of NKG2, a f
A;Reference number: PT0372; MUID:91178434;
                                                                                                                                                   natural killer cell receptor group N;Alternate names: NKG-C
                                                                                                                                                                                            RESULT 12
PT0374
     A;Residues:
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A;Residues: 1-266 <RES>
A;Cross references: EMBL:U10092; NID:g533491; PIDN:AAA50220.1;
C;Superfamily: natural killer cell receptor P1; C-type lectin |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 153, 1068-1079, 1994
A,Title: Ly-49 multigene family expressed by IL-2-activated A,Reference number: I49049; MUID:94300068; PMID:8027540
A,Recession: I49051
A,Status: preliminary; translated from GB/EMBI/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ly-49F-GZ antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revisio
C;Datesion: 149051
R;Smith, H.R.; Karlhofer, F.M.; Yokoy
J. Immunol. 153, 1068-1079, 1994
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;Molecule type: mRNA
;Residues: 1-231 <HOU>
                                                                                                                     ;Species: Homo sapiens (man);
;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text;
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                                                                                                                                                                                                                                                                                                                                                                                                                SCYGFFRHNLTWEBSKQYCTDMNATLLKIDNZNIVEYIKARTHLI---RWVGLSRQKSNE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMLTNRSIDSRPGNELLESLNR--
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23.7%;
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Pred. No. 1.6e-07;
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                                             family of related; PMID:2007850
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A;Note: sequence extracted from NCBI backbone C;Superfamily: C-type lectin homology F;256-377/Domain: C-type lectin homology <LCH>
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C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
C;Accession: A46274
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A46274
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A;Molecule type: nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:9787095
A;Map position: 12p13-12p13
C;Superfamily: natural killer cell
                                                                                                                                                                                                                                                                                                                                                 A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: glycoprotein; transmembrane protein F;71-96/Domain: transmembrane #status predicted F;27,100,149,178/Binding site: carbohydrate (Asr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X54869; NID:g35060; A;Experimental source: natural killer cell C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: KLRC2; NKG2-C
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                           Sest
                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100,149,178/Binding site: carbohydrate
                                                                                                                                                                                                                           Local
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   344
                                   187
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8
                                                                                                                                                                                                                                                                                                                                                1-404 <CUR>
                                                                                                                                                                                                                        Similarity
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NRGEPNNVGEEDCAEFSGNGWNDDKCNLAKFWICKKSAASCSRDE
                                                                CKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLESFKQYW
                                                                                                                                                                GTLQQLAKRECQYVVKQ-SELKGTEKGHKCSPCDTNWRYYGDSCYGFERHNLTWEESKQY 129
                                   EDGK--
                                                                                                  CTDMNATLLKI----DNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFL
                                                                                                                                    GELPEKSKQ--QEIYQELTQLKAAVE-RLCHPCPWEWTFFQGNCYFMSNSQRNWHDSITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMIYHCKHK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASILPSSWIGVFRNSSHHPWVTINGLAFKH---KIKDSDNAELNCAVLQVNRLKSAQCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGTFKGHKCSECDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLTAEVLGIIC----IVLMATVLKTIVLIPFLEQNNSSPNTRTQ
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KARHCGHCPESWITYSNSCYYIGKERRTWEESLLACTSKNSSLLSIDNESEIKFL-
                                -GNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQ
                                                                                                                                                                                                                                                                                                                                                                acid
                                                                                                                                                                                                                      13.0%;
23.0%;
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                                                                                                                                                                                                        37;
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                                                                                                                                                                                                    Score 164.5; DB 2;
Pred. No. 4.8e-07;
7; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 167; DB 2;
Pred. No. 1.5e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor
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                                                                                                                                                                                                                                                                            <HCH>
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                                                                                                                                                                                                                                                                                                          (NCBIN:113134,
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                                                                                                                                                                                                      Indels
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                                227
                                                                                                                                                                                                                                                                                                          NCBIP: 113135)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-Dec-1995
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a

natural killer (C;Species: Mus (C;Date: 02-Jul-

cell receptor Ly49C - musculus (house mouse) -1996 #sequence_revision

_revision 02-Jul-1996

#text_change

17-Mar-2000

mouse

RESULT

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Ly49H - mouse
C;Species: Mus
C;Date: 27-Feb
C;Accession: I
                                                                                                                                                                                                                                                                                                                                 R;Brennan, J.; Mager, D.; Jefferies, W.; Takei, F.
J. Exp. Med. 180, 2287-2295, 1994
A;Title: Expression of different members of the Ly-49 gene A;Reference number: 149114; MUID:95053763; PMID:7964501
A;Accession: 149114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
I49114
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R;Held, W.; Roland, J.; Raulet, D.H.
Nature 376, 355-358, 1995
A;Title: Allelic exclusion of Ly49-family genes encoding class I MHC-specific receptors
A;Reference number: I49361; MUID:95356819; PMID:7630404
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                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U12889; NID:g602407; PIDN:AAA58704.1; PID:g602408
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-266 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: SMBL:U34892; NID:g1003008; A;Accession: I49362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: I49363
A;Status: preliminary; translated from GB/EMBL/DD3J
                                                                                                                                                                                                                                                                                      A;Residues:
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A; Residues: 1-266 < RES>
                                                                                                                                                                                                              ;Superfamily: natural killer cell receptor P1; C-type lectin homology
                                                                                                                                                                                                                                                                                                Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Mus musculus (house mouse)
;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 19-May-2000;Accession: I49114
                                                                                                                                                     Matches
                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                      1-266 <RES>
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                                                                                                                                                                   Similarity
                 NLKEEMLTNKSIDCRPSYELLEYIKREQERWDSETKSVSDSSRDTGRGVKYWFCYGTKCY
                                                                                                               WRVMALILLILCVGMVVGLVALGIWSVMQ-RNYLQDENENRTGTLQQLAKRFCQYVVKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                    ELKG---TFKGHKCSPC--
                                                                                 WQLIVIALGILCSLRLV-IVAVFVTKFFQYSQHKQBINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIMNKTTWSGCKANCQHYSVPIVKIEDEDELKFL--QRHVIPESYWIGLSYDKKKKEWAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDBNENRTGTLQQLAKRFCQYVVXQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDGSVISENM----FEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLI---RWVGLSRQKSNEVWKW 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKEEMLTNKSIDCRPSNELLDYIKREQDRWNSETKTVLDSSRDTGRGVKHWFCYGTKCYY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKG---TFKGHKCSPC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WQLIVKALGILCFLLLVIVAVLTİKIFQYSQHKQEINE----TLNHYHN--CSNMQSDFN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                 12.7%;
21.2%;
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                                                                                                                                                  41;
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                                                                                                                                              Score 160.5; DB 2;
Pred. No. 6.8e-07;
1; Mismatches 79;
                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 163.5; DB 2;
Pred. No. 3.7e-07;
4; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- CVFLSKARIEDTDÖNI PYÝCI CGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g1003009
                                                                                 ---TLNH--RHNCSNMQRDF
                                                                                                                                                                               Length
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                                                                                                                                                Indels
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                                                  DIN-----WRYYGDSCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --NWRYYGDSCYG 115
                                                                                                                                                                                 266;
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                                                                                                                                                                                                                                                                                                                                                                  defines distinct natu
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - KLDKS
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hNKR-Pla protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
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J. Biol. Chem. 265, 11295-11298, 1990
A;Title: Molecular cloning and sequence analysis of cDNA encoding A;Reference number: A42230; MUID:90293078; PMID:2358462
A;Accession: A42230
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A42230
                                                                                                                                                                    A;Cross-references: EMBL:Ull276; NID:g538270; PIDN:AAA21605.1; C;Superfamily: natural killer cell receptor P1; C-type lectin F;94-210/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                    R;Lanier, L.L.; Chang, C.; Phillips, J.H.
Jimmunol. 153, 2417-2428, 1994
A;Title: Human NRR-PIA: A disulfide-linked homodimer of A;Reference number: I38700; MUID:94358407; PMID:8077657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:J05495; NID:g204302; PIDN:AAA41216.1; C;Superfamily: hepatic lectin; C-type lectin homology F;175-298/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lectin M-ASGP-BP precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change
                                                                                                                                                                                                                                   A; Residues: 1-225 < RES>
                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                            A; Status: preliminary; translated
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A; Residues: 1-306 < II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A42230
R;Ii, M.; Kurata, H
                                                                                       Matches
                                                                                                       Query Match
Best Local :
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                          1 MQDEDGYITLNIKTRKPALVSVGPASS---
                                                                                                          Similarity
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  MDQQAIYAELNLPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGMTKVDQLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDRVQQLGKDLKTLTCQLASLKNNGSAVAC--CPLHWMEHEGSCYWFSQSGKPWPEADKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -306 <IIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFIMNKTTWSGCKANCQHYSVPIVKIEDEDELKFL--QRHVILESYWIGLSYDKKKKEWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFFRENLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLI---RWVGLSRQKSNEVWK 171
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLDKFP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
                                                                                                       12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNMNCAYF-HNGKMHPTFCENKGYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THNGQSKLDMKIKKMNFTSRGCVFLSKARIEDTDCNTPYYCICGK-
                                                                                 43;
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Pred. No. 8e-07;
Wismatches 72;
                                                                                                       Score 158; DB 2;
Pred. No. 9.5e-07;
-DSGPESSSPSSLPRDVCQGSPWHQFALKLSCAGIILLVLV
                                                                                                                                                                                                                                                                                from
                                                                                     Mismatches
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                                          --FWWRVMALIL---LILCVGM
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                                                                                                                         Length 225;
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Gaps

9

-RL

257 225 206 168 150

113 90

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RESULT 18
149049
Ly-49D-GE antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision
C;Accession: 149049
R;Smith, H.R.; Karlhofer, F.M.; Yokoyam
J. Immunol. 153, 1068-1079, 1994
                                            natural killer cell receptor Ly49A - mouse C. Species Mus musculus (house mouse)
C. Date: 02-Unl-1996 #sequence_revision 02-,
C. Accession: 149361
R. Held, W.; Roland, J.; Raulet, D.H.
Nature 376, 355-358, 1995
A; Title: Allelic exclusion of Ly49-family of A. Reference number: 149361; MUID:95336819;
                                                                                                                                                                            RESULT 19
I49361
 A;Accession: I49361
A;Status: preliminary; translated
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Nolecule type: mRNA

A;Residues: 1-260 <RES>

A;Cross-references: EMBL:U10090; NID:g533487; PIDN:AAA50218.;

C;Superfamily: natural killer cell receptor P1; C-type lectin;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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H.R.; Karlhofer, F.M.; Yokoyama,
                                                                                                                                                                                                                                                                                                     187
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                                                                                                                                                                                                                                                                                                  VVPSDSCWIGLSYDNKKKDWAWIDNRPSKLALNTTKYNIRDG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETRKPEKARLRVP----WQ-----LIVIALGILISLRLVTVAVLMINIFQ--YGQQKHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTRKPALVSVGPASSFWWRVMALILLILCVGMVVGL----VALGIWSVMQRNYLQDENEN
                                                                                                                                                                                                                                         CDQSFICICGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTGTLQQLAKRFCQYVVKQSE--LKGTFKGHKCSPC-----DTN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NWRYYGDSCYGFFRHNLT-WEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                          -LKEFLKHHNNCSIMOSDINLKDELLKNKSIECNLLESLNRDQNILCDKTRTVLDYL 130
                                                                                                                                                                                                                                                                                                                   -RWVGLSRQKSNEVWKWEDG--SVISENMFEF-LEDGKGNMNCAYFHNGKMHPTF 207
                                                                                                                                                                                                                                                                                                                                                                                           WRYYGDSCYGFFRHNLTWEESKOYCTDMNATLLKIDNRNIVEYIKARTHL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%;
                                                                                                                                                                                                                                         -RLDKFP
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                  from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 158; DB 2;
Pred. No. 1.1e-06;
B; Mismatches 83
                                                                                                                                                                                                                                         259
                                                                                                                                                                                                                                                                      229
                                                                                                                      02-Jul-1996 #text_change
                                               genes encoding; PMID:7630404
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                                                           class I MHC-specific receptors
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RESULT
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
C;Accession: 149059
C;Accession: 149059
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-266 <RESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wong, S.; Freeman, J.D.; Kelleher, C.; Mager, D.; Takei, F. J. Immunol. 147, 1417-1423, 1991
A;Title: Ly-49 multigene family: New members of a superfamily A;Reference number: I49058; MUID:91332459; PMID:1869832
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A;Cross-references: EMB
C;Superfamily: natural
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                                                                                                                                                                                                                                                                                                                                                                            53;
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                       IDNGPSKLDMKIRKMNFKSRG--
                                                                                                                                                  EDGSVISENM----FEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQL
                                                                                                                                                                                                                                                                                LKG---TFKGHKCSPC
                                                                                                                                                                                                                                                                                                                                        WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVXQSE
                                                                                                                                                                                   FIMNKTTWSGCKANCQHFSVPILKIEDEDELKFL-
                                                                                                                                                                                                              FFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLI---RWVGLSRQKSNEVWKW
                                                                                                                                                                                                                                              LKEEMLTNKSIDCRPSNETLEYIKREQDRWDSKTKTVLDSSRDTGRGVKYWFCYSTKCYY
                                                                                                                                                                                                                                                                                                          WQLIVKALGILCFLLLVTVAVLAVKIFQYNQHKQBINE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWKWEDG---SVISENMFEF-LEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFWWRVMALILLILC--VGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYV 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGFFRHNLTWEESKOYCTDMNATLLKIDNRNIVEYIKARTHLI----RWVGLSRQKSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKQSELKGTFKGHKCSPCD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nces: EMBL:U34890; NID:g1003004; PIDN:AAA,77065.1; PID:g1003005 natural killer cell receptor P1; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                          33;
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                                                                                                                                                                                                                                                                                                                                                                    Score 157.5; Db 2,
Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 157.5; DB 2;
Pred. No. 1.2e-06;
37; Mismatches 91;
                                                                                                                    -CVFLSKARIEDIDCNIPYYCICGK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                 -QRHVIPENYWIGLSYDKKKKEWAW
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 266;
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264

228 214 172 156 115 96 89 Gaps

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 102-120/137', X', 139-151 <ODA>
A;Residues: 102-120/137', X', 139-151 <ODA>
C;Superfamily: hepatic lectin; C-type lectin homology
C;Keyworts: glycoprotein; lectin; macrophage; transmembrane protein
C;Keyworts: glycoprotein; lectin; macrophage; transmembrane protein
C;Heffeld: C-type lectin; homology C:CH>
F;173-296/Domain: C-type lectin;homology C:CH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: JX0209; MUID:92268032; PMID:1587794 A;Accession: JX0209
    A;Reference number: A46502; MUID:92388663; A;Accession: A46502 A;Status: preliminary
                                                           J. Immunol. 149, 1957-1963, A; Title: Genomic structure
                                                                                                   A;Cross-references: GB:M77676; NID:g200058
A;Experimental source: A-LAK cells, C57BL
A;Note: sequence extracted from NCBI backbone
R;Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A46467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S36676; NID:g249360; PIDN:AAB22171.1; R;Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T. J. Biochem. 104, 600-605, 1988
                                                                                                                                                                                                                                        J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kil
A;Reference number: A46467; MUID:91349596; PMID:1880421
                                                                                                                                                                                                                                                                                                     C;Date: 18-Jun-1993 #sequence_revision 19-Feb-1999 #text_change C;Accession: A46467; A46502; A46456 R;Giorda, R.; Trucco, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 'MHLLCT', 1-227 <GIO>
                                                                                                                                                                                                                                                                                                                                             N;Alternate names: NKR-P1 protein
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revisio
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;Species: Mus musculus (house mouse)
;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
;Accession: JX0209; PX0009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Molecule type: mRNA
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hem. 111, 331-336, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFEKGFKNWAPLQPDNWFGHGLGGGEDCAHITTGGPWNDDVCQRTFRWICEMK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKAR-THLIRWVGLSRQKSNEVWKWEDGS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REQALKIDLSDLIDHVQQLRKDLKALTCQLANLKN--NGSEVACCPLHWIEHEGSCYWFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRNYLQDBNENRTGTLQQLAKRFCQYVVKQSELXGTFKGHKCSPCDTNWRYYGDSCYGFF
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                                                           1957-1963, 1992
structure and strain-specific
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                                                                                                 E.P.; Ip,
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Pred. No. 1.5e-06;
:4; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                        mouse
                                                                                                   T.K.; Trucco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KGNMNCAYF-HNGKMHPTFCENKHYLMCERK
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A; Molecule Lype; MAN
A; Residues: 1-109/M; 1/111-181, 'D', 183-227 <GI2>
A; Cross-references: GB:X64716; NID:g53395; PIDN:CAAA5971.1; PID:g817989
A; Cross-references: GB:X64716; NID:g53395; PIDN:CAAA45971.1; PID:g817989
A; Cross-references: GB:X64716; NID:g15395; PIDN:CAAA45971.1; PID:g817989
A; Cross-references: BALB/C 3T3 fibroblastoid cell line
A; Note: sequence extracted from NCBI backbone (NCBIN:113067, NCBIN:131063, NCBI
A; Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.I
J. Immunol. 147, 3229-3236, 1931
A; Title: CDNA cloning of mouse NKR-Pl and genetic linkage with LY-49. Identific
A; Reference number: A46456; MUID:92013158; PMID:1680927
A; Reference number: A46456; MUID:92013158; PMID:1680927
A; Accession: A46456
A; Molecule type: mNAA
A; Residues: 1-38, 'L', 40-227 <YOK>
A; Cross-references: GB:M77753; NID:g198569; PIDN:AAA39366.1; PID:g198570
A; Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)
C; Superfamily: natural killer cell receptor P1; C-type lectin homology
F; 94-210/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell surface glycoprotein YE1/48 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfami.
C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M25812; NID C;Superfamily: natural killer cell
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A; Residues: 1-262 < YOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A murine T lymphocyte antigen belongs to a supergene A;Reference number: A45813; MUID:89309828; PMID:2787364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Yokoyama, W.M.; Jacobs, L.B.; I
J. Immunol. 143, 1379-1386, 1989
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A; Residues: 1-109, 'H
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Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                         52;
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                                                                                                      YGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLI--
                                                                                                                                                                                                     VKQSELKGTFKGHKCSPCD-
                                                                                                                                                                                                                                               SFHWKFIVIALGIFCFLLLVAVSVLAIKIFOYDQQKKLQBFLNHHNN
                                                                                                                                                                                                                                                                                                    SFWWRVMALILLILC--VGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNSF-WIGERYTLPDMNWKWINGSTLNSDVLKITGDTE-NDSCAAISGDKVTFESCNSDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNWNCAYFHNGKMHPTFCENKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAKLECPQBWLSHRDKCFHVSQVSNTWEEGLVDCDGKGATLMLIQDQBELRFLLDSIKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDN----RNIVEYIKAR 152
VWKWEDG--SVISENMFEF-LEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKV 225
                                                  YYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFLQ----LVVPSDSCWVGLSYDNKKK
                                                                                                                                                   QSDINLKDEMLKUKSMECDLLESLNRDQNRLYNKTKTVLDSLQHTGRGDKVYWFCYGMKC 150
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24.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanagawa, C.;
                                                                                                                                                                                                                                                                                                                                                   Score 152.5; DB 2
Pred. No. 3.5e-06;
8; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 156; DB 2;
Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ):g191979;
receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:AAA37242.1; PID:g309108
P1; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shevach, E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                      91;
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                                                                                                    --RWVGLSRQKSNE 168
                                                                                                                                                                                                                                                                                                                                                                                                        262;
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                                                                                                                                                                                                     TNWRYYGDSC
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                                                                                                                                                                                                                                                       --CSNM
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W.E.
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P

oup 2-C, splice form 2 - human evision 07-Jun-1996 #text_change 19-May C.; Bach, F.H.; Houchins, J.P. Clike receptors have divergent carboxy-t D:94102823; PMID:8276468 D:94102823; PMID:8276468	ell receptor Pl; C-type lectin homology; Score 151.5; DB 2; Length 240;	tch 12.0%; Score 151.5; DB 2; Length 240; al Similarity 24.7%; Fred. No. 3.9e-06; 42; Conservative 26; Mismatches 73; Indels 29; Gaps 31 RVMALILLICVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQCLAKRFCQYVVXQSEL 9	31 70	SKQYCTDMN-ATLLKIDNRNIVBYI 14	Qy 150 KARTHLIRWYGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFH 199	RESULT 25 I49050 Ly-49E-GE antigen - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000 C;Accession: I49050	R;Smith, H.R.; Karlhofer, F.M.; Yokoyama, W.M. J. Immunol. 153, 1068-1079, 1994 A;Title: Ly-49 multigene family expressed by IL-2-activated NK cells. A;Reference number: 149049; MUJD:94300068; PMJD:8027540 A:Accession. 149050	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-266 <res> A;Cross-references: EMBL:U10091; NID:g533489; PIDN:AAA50219.1; PID:g533490 C;Superfamily: natural killer cell receptor P1; C-type lectin homology</res>	Query Match 12.0%; Score 151.5; DB 2; Length 266; Best Local Similarity 20.7%; Pred. No. 4.4e-06; Matches 50; Conservative 38; Mismatches 94; Indels 59; Gaps 9;	QY 30 WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSE 89 :: :: : :	QY 90 LKGTFKGHKCSPCD	RESULT 24 RESULT 24 RATURAL Killer ce C; Species: Homo s C; Species: Homo s C; Date: 07-Jun-19 C; Accession: I545 R; Adamkiewicz T; File: Natural A; Reference number A; Accession: I545 A; Const. = Ference cuber A; Const. = Ference c; Species: Homo s C; Species: Mis murch Best Local Simi Matches 42; Qy 31 RVM Qy 31 RVM Qy 31 RVM Qy 31 RVM C; Superfamily: na Query Match Best Local Simi Matches 42; Qy 31 RVM Qy 31 RVM Qy 31 RVM C; Species: Mus murch Best Local Simi Matches 42; Qy 31 RVM Qy 31 RVM Qy 31 RVM C; Db 110 Qy 91 KGT Db 110 Qy 150 KAR Db 110 Qy 150 KAR A; Title: Ly-49 mulch B; Accession: I490 C; Accession: I490 A; Reference number A; Reference number A; Residues: 1-266 A; Cross-reference C; Superfamily: nai Query Match	an proup 2-C, splice form 2 - human no_revision 07-Jun-1996 #text_change 19-May-2000 rry, C.; Bach, F.H.; Houchins, J.P. property, C.; Bach, J.P. property, C.; Bach, J.P. proper
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IgB Fc receptor, low-affinity - mouse

NAlternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IgE receptor

C;Species: Mus musculus (house mouse)

C;Date: l2-Feb-1993 #sequence_revision 28-Oct-1994 #text_change 22-Jun-1999

C;Accession: A43518; A33840

R;Gollnick, S.O.; Trounstine, M.L.; Yamashita, L.C.; Kehry, M.R.; Moore, K.W.

J. Immunol. 144, 1974-1982, 1990

A;Title: Isolation, characterization, and expression of cDNA clones encoding the mouse
A;Reference number: A43518; MUID:90171598; pMID:2137845

A;Accession: A43518

A;Molecule type: mRNA
A;Residues: 1-331 <GOL>
A;Cross-references: GS:M34163; NID:g193242; PIDN:AAA37603.1; PID:g309227
R;Bettler, B.; Hofstetter, H.; Rao, M.; Yokoyama, W.M.; Kilchherr, F.; Conrad, D.H.
Proc. Natl. Acad. Sci. U.S.A. 86, 7565-7570, 1989

A;Title: Molecular structure and expression of the murine lymphocyte low-affinity recep
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
LNMSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-284 <TAK>
A;Residues: 1-284 <TAK>
A;Cross-references: EMBL:D13517; NID:g220480; PIDN:BAZ
C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: glycoprotein; transmembrane protein
F;153-276/Domain: C-type lectin homology <LCH>
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R;Takezawa, R.; Shinzawa, K.; Watanabe, Y.; Akaike, T.
Biochim. Biophys. Acta 1172, 220-222, 1993
A;Title: Determination of mouse major asialoglycoprotein receptor cDNA sequence.
A;Reference number: S29855; MUID:93176818; PMID:8439566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 VISENMFEFLEDGK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 QQKDLTEDHSSLLLHVKQLVSDVRSLSCQMAAFRGNGSERTC--CPINWVEYEGSCYWFS 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKEEMLRNKSIDCSPGEELLESLNREQNRWYSETKTDLDSSQDTGTGVKHWPCYGTKCFY
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24.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 151; DB 2; L
Pred. No. 5.2e-06;
3; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CIFLSKTRLEDÍNČNŃSYFCIČGK---
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A;Reference number: A33840; MUID:90017519; PMID:2529542
A;Accession: A33840
A;Accession: A33840
A;Molecule type: mRNA
A;Residues: I-331 <ABTS
A;Cross-references: GB:M93371; NID:g193245; PIDN:AAA74898.1; PID:g193246; GB:M27150
C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic
f B-cells.
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
C;Superfamily: IgE receptor II; C-type lectin homology
F;1125/Domain: transmembrane #status predicted <INT>
F;14-22/Region: Stop-transfer sequence
F;26-46/Domain: transmembrane #status predicted <TMM>
F;47-331/Domain: extracellular #status predicted <EXT>
F;66-86/Region: 21-residue repeat
F;108-128/Region: 21-residue repeat
F;108-128/Region: 21-residue repeat
F;108-128/Region: 21-residue repeat
F;186-305/Domain: C-type lectin homology <LCH>
F;65,114/Binding site: carbohydrate (Asn) (covalent) #status predicted
A;Molecule type: mRNA
A;Residues: 1-86,90-220 <RYA>
A;Residues: 1-86,90-220 <RYA>
A;Cross-references: GB:343141; NID:9254094; PIDN:AAB22979.1; PID:9254095
A;Experimental source: C57BL/60 NK cells
A;Experimental source: C57BL/60 NK cells
C58uperfamily: natural killer cell receptor P1; C-type lectin homology
C;Keywords: transmembrane protein
F;91-207/Domain: C-type lectin homology <LCH>
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A;Experimental source: NK cells, C57BL7B
A;Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBIP:52383)
A;Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBIP:52383)
B;Ryan, J.C.; Turck, J.; Niemi, E.C.; Yokoyama, W.M.; Seaman, W.3.
J. Immunol. 149, 1631-1635, 1992
A;Title: Molecular cloning of the NK1.1 antigen, a member of the NKR-P1 family of natural A;Reference number: A46499; MUID:92373004; PMID:1506685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKR-P1 protein homolog gene-40 - mouse N;Alternate names: natural killer cell activation molecule; NKI.1 alioantigen C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999 C;Accession: C46467; A46499
R;Giorda, R; Trucco, M.
J. Immunol. 147; 1701-1708, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Immunol. 147, 1701-1708, 1991
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kil A;Reference number: A46467; MUID:91349596; PMID:1880421
A;Accession: C46467
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-220 <GIO>
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSRQKSNEVWKWEDGSVISENMFEFLEDGKGNM--NCAYFH-NGKMHPTFCENKHYL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRLQDDLVNIKSLGLNEKRTASDSLEKLQBEVAKLWIEILIS-----KGTACNICPK 188
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Pred. No. 6.2e-06;
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C;Accession: T28141 C;Accession: T28141 S,Milne, S.; Kaufman, J.; Beck, S. submitted to the EMBL Data Library, May 1998 N.Description: DNA sequencing and analysis of the

chicken major histocompatibility comp

#text_change 15-Oct-1999

C type lectin, B locus - chicken C;Species: Gallus gallus (chicken) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999

RESULT T28141

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A; Residues: 1-262 < CHA>
C; Superfamily: natural )
C; Keywords: glycoprotei:
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C;Date: 18-Apr-1989 #sequence_revision 18-Apr-1989 #text_change 19-May-2000
C;Accession: A30573
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J. Immunol. 142, 1727-1736, 1989
A;Title: Molecular cloning and characterization of a no-
A;Reference number: A30573; MUID:89140367; PMID:2783949
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                                                          AWIDNRPSKLALNTGKYNIRDG----GCMLLSKTRLDNGNCDQVFICICGK---
                                                                                       KWEDG--SVISENMEEF-LEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQ
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                                                                                                                                                                                                             QSELKGTFKGHKCSPCD-
                                                                                                                                                                                                                                       SPHWKFIVIALGIFCFLLLVAVSVLAI-----KIFQYDQQKNCEEFLNH--HNNCSNMQS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKYNSF-WIGLRFTLEDMNWKWINGTTFNSDVLKITGVTENG----SCASILGDKVTPES 198
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                                                                                                                   FVMDRKTWSGCKQACQSSSLSLLKIDDEDELKFLQ-
                                                                                                                                                FFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLI-----RWVGLSRQKSNEVW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N----LECPQDWLLHRDKCFHVSQVSNTWEEGQADCGRKGATLLLIQDQEELRFLLDSIK 143
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21.5%;
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                                                                                                                                                                                                                                                                                                 Score 149.5; DB 2;
Pred. No. 6.5e-06;
6; Mismatches 95;
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Pred. No. 5.4e-06;
3; Mismatches 78;
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A;Molecule type: mRNA
A;Residues: 1-23,43-81,87-311 <PAIS
A;Residues: 1-23,43-81,87-311 <PAIS
A;Coss-references: EMBL:X55283; NID:g34354; PIDN:CAA38997.1; PID:g34355
R;Yuk, M.H.; Lodish, H.F.
Cell Biol. 123, 1735-1749, 1993
A;Title: Two pathways for the degradation of the HZ subunit of the asialon for the degradation of the HZ subunit of the asialon for the degradation of the HZ subunit of the asialon for the HZ subunit of the asialon for the degradation of the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the asialon for the HZ subunit of the AZ subunit of the AZ subunit of the HZ subunit of the AZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ subunit of the HZ s
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R;Paietta, E.; Stockert, R.J.; Racevskis, J.
Hepatclogy 15, 395-402, 1992
A;Title: Differences in the abundance of variably spliced transcripts for the A;Reference number: I37995; MUID:92184202; PMID:1371982
A;Reference number:
A;Accession: A49466
A;Molecule type: pro
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A; Residues: 69-81,87-99 <L
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A; Residues: 69-99 < LED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A39100; MUID:91093236; PMID:1985943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 10-Dec-1999
C;Accession: A2319; A39100; E39100; I37995; A49466; B49466; S14525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asialoglycoprotein receptor H2a - human
N;Alternate names: hepatic lectin H2a
N;Contains: ASGPR; asialoglycoprotein receptor H2a; asialoglycoprotein receptor H2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-311 <SPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A25179; MUID:86016723; PMID:3863106
A;Accession: A25179
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A;Title: Sequence of a second human asialoglycoprotein receptor: conservation
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A;Accession: T28141
A;Status: preliminary; translated
A;Molecule type: DNA
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25.4%;
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Pred. No. 5e-06;
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                                                                   PMID:8276894
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Repartic lectin - rat

RyAlternate names: ASGF; asialoglycoprotein receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Feb-1986 #sequence revision 04-Dec-1986 #text_chan;

C;Accession: A92497; A94020; B94020; A54727; A03166

R;Leung, J.O.; Holland, E.C.; Drickamer, K.

J. Biol. Chem. 260, 12523-12527, 1985

A;Title: Characterization of the gene encoding the major rat A;Reference number: A92497; MUID:86008335; PMID:2995379

A;Accession: A92497
A,Title: Isolation and expression of cDNA clones A;Reference number: A54727; MUID:87026895; PMID:2 A;Accession: A54727 A;MOlecule type: mRNA A;Residues: 12-284 <WAT'> A;Cross-references: GB:M21770; NID:g202985; PIDN: A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-284 <LEUS
A;Cross-references: GB:KU2817; NID:g206646; PIDN:AAA42037.1;
R;Holland, B.C.; Leung, J.O.; Drickamer, K.
Proc. Natl. Acad. Sci. U.S.A. 81, 7338-7342, 1984
A;Title: Rat liver asialoglycoprotein receptor lacks a cleava
A;Reference number: A34020; MUID:85063786; PMID:6095287
                                                                                                                                                                     A;Note: cione 22 codes
R;Watts, C.
Biosci. Rep. 6, 527-534
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 92-284 <HO2>
                                                                                                                                                                                                                                                                                       A; Experimental source: clone A; Accession: B94020
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A;Residues: 1-60,'R',62-210 <HOL>
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C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: alternative splicing; endocytosis; glycoprotein; lectin; liver; phosphoprote; l-311/Product: asialoglycoprotein receptor H2a #status predicted <MATI>
F;1-81,87-311/Product: asialoglycoprotein receptor H2b #status predicted <MAT2>
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F;1-22,43-81,87-311/Product: asialoglycoprotein receptor H2c #status predicted <MAT3>
F;59-78/Domain: transmembrane #status predicted <TMM>
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A;Accession: B49466
A;Molecule type: protein
A;Residues: 87-98 <YU2>
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A;Cross-references: GDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 QYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKID 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                  B94020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMNCAYEH-NGKMHPTFCENKHYLMCERKAGMT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWEEQXFIVQHTNPFNTWIGLT--DSDGSWKWVDGTDYRHNYKNWAVTQPDNWHGHELGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFVACQMELLHS-NGSQRTCCPVNWVEHQGSCYWFSHSGKAWAEAEKYCQLENAHLVVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEDCVEVQPDGRWNDDFCLQVYRWVCEKRRNAT
                                                                                                                                                                   527-534, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                               for a terminator
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26.1%;
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                                                                                                                                                                                                                                                                                                          22;
                   NID: g202985; PIDN: AAA40764.1;
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                                                                                                                                                                                                                                                                                                             clone
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Pred. No. 1.6e-05;
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                                                                                                                    PMID:2945599
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                                                                                                                                       for a
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                 PID:g202988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g206647
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                                                                                                                                  asialoglyccprotein
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A;Cross-references: BMBL:U10094; NID:g533495; PIDN:AAA50222.1; PID:g533496
R;Brennan, J.; Mager, D.; Jefferies, W.; Takei, F.

J. Exp. Med. 180, 2287-2295, 1994
A;Title: Expression of different members of the Ly-49 gene family defines day;Reference number: I49114; MUID:95053763; PMID:7964501
A;Accession: I49115
A;Accession: I49115
A;Kotatus: preliminary; translated from GB/EMBL/DD5J
A;Molecule type: mRNA
A;Residues: 1-43, Q',45-267 <RE2>
A;Cross-references: EMBL:U12890; NID:g602409; PIDN:AAA58705.1; PID:g602410
C;Genetics:
A;Gene: Ly49G.4
C;Superfamily: natural killer cell receptor P1; C-type lectin homology
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                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ly-49G.2 antigen mouse
N;Alternate names: Ly-49E
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_cha
C;Accession: I49053; I49115
C;Accession: Karlhofer, F.M.; Yokoyama, W.M.
R;Smith, H.R.; Karlhofer, F.M.; Yokoyama, W.M.
J. Immunol. 153, 1668-1079, 1994
A;Title: Ly-49 multigene family expressed by IL-2-activated
A;Reference number: I49049; MUID:94300068; PMID:8027540
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A;Status: preliminary; translated
A;Molecule type: mRNA
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F;61-284/Domain: extracellular #status predicted <EXYI>
F;153-276/Domain: C-type lectin homology <LCH>
F;153-276/Binding site: carbohydrate (Asn) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-267 < RES>
                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 57
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Best Local /
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    117
                                                     103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                            Similarity
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                                                RNKSIECRPGNDLLESLSRDQNRW--
FRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIX-ARTHLIRWVGLSRQKSNEVWKWEDG
                                                                                                                                                                                       WRVMALILLILC--VGMVVGLVALGIWSVMQRNY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWTEADXYCQLENAHLVVVTSWBEQRFVQQHMGPLNTWIGLTDQ--NGPWKWVDGTDY-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWEESKQYCTDMNATLLKIDNRNIVEYIKART-HLIRWVGLSRQKSNEVWKWEDGSVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LREDHSRLLLHVKQLVSDVRSLSCQMAALRGNGSERIC--CPINWVEYEGSCYWFSSSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LODENENRIGILOQLAKRECOYVVKQSELKGIEKGHKCSPCDINWRYYGDSCYGFFRHNL
                                                                                                                                      WKLIVIACGILCFLLLVTVALLAITIFQHSQQKHELQETINCHDNCSPTQSDVNLKDELL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGFKNWRPGQPDDWYGHGLGGGEDCAHFTTDGHWNDDVCRRPYRWVCETELG
                                                                                          -NENRTGT---LQQLAKRFCQYVVKQSELKGTFKG---HKCSPCDTNWRYYGDSCYGF
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                      42; Mismatches
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                                                                                                                                                                                                                                                       Score 145;
Pred. No. 1
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Pred. No. 1.6e-05;
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                                            -YSETK-TFSDSSQHTGRGFEKYWFCYGIKCYYF
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                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                             Length 267;
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A;Reference number: A49707; MUID:94124484; PMID:8294398
A;Accession: A49707
                                                                                                                                                                                                                                                                              R;Lambeau, G.; Ancian, P.; Barhanin, J.; Lazdunski, M. J. Biol. Chem. 269, 1575-1578, 1994
A;Title: Cloning and expression of a membrane receptor.
                                                                                                                                                                                                                                                                                                                                          phospholipase A2 receptor precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: A49707
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A; Residues: 1-288 < RES>
A; Cross-references: EMBI
C; Superfamily: natural )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_c
C;Accession: I49015
R;Wong, S.; Freenan, J.D.; Kelleher, C.; Mager, D.; Takei,
J. Immunol. 147, 1417-1423, 1991
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A;Title: Ly-49 multigene family: New members of a superfamily
A;Reference number: I49058; MUID:91332459; PMID:1869832
                                                                                                                                                                                                                             A;Status: preliminary
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A;Status: preliminary; translated
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Best Local S
Matches 49
                                                                         ;956-1094/Domain: C-type
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156
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                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEDGSVISENMFEFLEDGKCN-----MNCAYFHNGKMHPTFCENKHYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYYFIMDDKKWNGCKQICQDYNLTLLKTNDEDELKFLKSQLQRNTYWISLTHHKSK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WKFIVIVLGILCFLLLTVAVLVIHIFRDGQEKHEQEK-----TLNNLRQEY-QVMKND 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYGFFRHNLTWEBSKQYCTDMNATLLKIDNRNIVEYIKARTHL-IRWVGLSRQKSNEVWK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSIMEEMLRNKSSECKALNDSLHYLNREQNRCLRKTKIVLDCSQNKGKQVEGYWFCCGMK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SVISENMEEF-LEDGKGNWNCAYFHNGKWHPTFCENKHYLMCERKAGWTKVDQLP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMDRKTWSGCKQTCQISSLSLLKIDNEDELKFLQNLAPSDISWIGLSYDNKKKJWVWIDN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -BESQQIGDRPSK-LDSAARNSVPNRQKCAYLSSFSTEEDDCARTHGCICEKR
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21.0%;
11.4%; Score 143.5; DB 1; 23.7%; Pred. No. 0.00015; tive 32; Mismatches 82;
                                                                         lectin homology <LCH2>
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8 د
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Pred. No. 2.3e-05;
B; Mismatches 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB/EMBL/DDBJ
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                                 Length 1458;
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A;Cross-references: EMBI
A;Experimental source: g
C;Genetics:
A;Gene: CESP:C25B8.4
A;Map position: X
A;Introns: 74/1; 104/3;
                                                                                                     submitted to the EMBL Data Library, Decemb A; Description: The sequence of C. elegans A; Reference number: 221479
A; Accession: T34115
A; Status: preliminary; translated from GB/A; Molecule type: DNAA; Residues: 1-262 < WILD
                                                                                                                                                                                                                                                           hypothetical protein C25B8.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t.
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C;Species
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R;Smith, H.R.; Karlhofer, F.M.; Yokoyama, W.Y.
J. Immunol. 153, 1068-1079, 1994
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I49052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:U10093; NID:g533493; PIDN:AAA59221.1; C;Superfamily: natural killer cell receptor P1; C-type lectin h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Ly-49 multigene family expressed by IL-2-activated A;Reference number: I49049; MUID:94300068; PMID:8027540 A;Accession: I49052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-280 < RES>
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                                                                                                                                                                                                                                                       Accession: T34115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Mus musculus (house mouse)
;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000
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74/1; 104/3; 152/3; 195/2
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53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  KAGMTKVDQLP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYDNKKKDWVWIDNGPSKLALNTTKYNIRDGL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRQKSNEVWKWEDG--SVISENMFEF-LEDGKGNMNCAYFHNGKWHPTFCENKHYLMCER 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKYWFCYGIKCYYFNMDRKTWSGCKQTCQISSLSLLKIDNEDELKFLQNLAPSDISWIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DINWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIK-ARTHLIRWYGL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKSIECRPGNDLLESLSRDQNRWYSETKIFSDSSQHTGVHERPISKAEGKGRGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WKLIVIACGILCFLLLVTVALLAITİFQHSQQKHELQETLNCHDNCSPTQSDVNLKDELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRVMALILLILC--VGMVVGLVALGIWSVMQRNY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSFEWSNGSSVIFTNWHTLEPQIFPNRSQLCVSAEQSEGHWKVTDCEETHFYVCKK 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLQKEEKTWNEALHSCLSSNSTLIDIGSLAEVEFLVTLLGNENASET----WIGLSSNTF 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEVWKWEDGSVISENWFEFLED---GKGNMNCAYFENGKMH--PTFCENKHYLMCER 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                               EMBL:U41556; PIDN:AAC70872.1; GSPDB:GN00028; ce: strain Bristol N2; clone C25B8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 141.5; DB 2
Pred. No. 3.7e-05;
5; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                                                                                              December 1995
                                                                                                                                          GB/EMBI/DDBJ
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                                                                                                                                                                                             cosmid
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                                                                                                                                                                                             C25B8
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                                                                                    CES2:C25B8
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1487 <AIG>
A;Cross-references: GB:D30779; NID:g1375042; PIDN:BAA06443.1; PID:g691754
A;Cross-references: GB:D30779; NID:g1375042; PIDN:BAA06443.1; PID:g691754
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type
F;181-222/Domain: fibronectin type II repeat homology <2F1>
F;380-503/Domain: C-type lectin homology <LCH>

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A;Reference number: A;Accession: \$48719

regions

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phospholipase-A

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phospholipase-A(2) receptor protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S48719
                     Eur. J. Biochem. 225
A; Title: Structural
                                                R;Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita
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A;Introns: 33/2; 72/1; 227/3; 240/3; 274/1; 328/3; 350/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z82288; PIDN:CAH05324.1; GSPDB:GN00022; CESP:ZK896
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A;Status: prelimina
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A;Reference number: Z20466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G;Species: Caenorhabditis elegans
G;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28081
R;Barlow, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ZK896.7 - Caenornabditis elegans
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Best Local :
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Best Local Similarity
Matches 53; Conserv
                                       . Biochem. 225,
                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CESP: ZK896.7
                                                                                                                                                                                                                                        160 GLSROKSNEVWKWEDGSVISENWFEFLEDGKGNMNCAYFHNGKMHFTFCENK 211
                                                                                                                                                                                                                                                                                                                     107
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                         GLSRKKDYELFNWDDGTIVSYTNFEAGFPNKQDFVAENVRNGRWQ-TLAEHK
                                                                                                                                                                                                                                                                                                            RYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYI--KARTHLIR-----WV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNATLLKIDNRNIVEYIKARTHL----IRWVGLSR----QKSNEVWKWEDGSVISENMFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLIRPYKPVSNGWSALANCAAHPSAAINWDASAYTYFQP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNATLFVVNSQD--EWDAVREHFPQTGYTWIGLVRFTHFEKSQDAPIWQTEGAVNPTRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFRIFKLVLLVAAVGFVSTRFAQVKLENWSYKDFGTNAFTDISLDQRQHYHD---FPTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WWRVMALILLILCYGMY---VGLVALGIW-----
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
5, 375-382, 1994
comparison of phospholipase-A(2)-binding
S48719; MUID:95010128; PMID:7925459
                                                                                                                                                                                                                                                                                                                                                                      11.1%;
29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%;
22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZK896
                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                Score 140; DB 2
Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                              Pred. No. 7e-(
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 141; DB 2;
Pred. No. 3.8e-05;
%1; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CPDGWVRFSDSCYWIEQHKQSFAEAEKRCYE
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFHNGKMHPTFCENKHYLMCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 262;
                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SVMQRNYLQDENENRTGT
                                                                                                                                                                                                                                                                                                                                                                                   . 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CSFKFYSICER
                                                                                    20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
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F;79,147/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 17p13-17p11

C;Superfamily: hepatic lectin; C-type lectin homology
C;Keywords: endocytosis; 91ycoprotein; lectin; phosphoprotein; receptor; transmembrane
F;2-291/Product: hepatic lectin H1 #status predicted <MAT>
F;2-40/Jomain: intracellular #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M10058; NID:gl79078; PIDN:AAA51785.1; PID:gl79079 C;Comment: This receptor is expressed in mammals exclusively in hepatic particular of c;Comment: By homology with the R1 receptor, the initiator Met is removed C;Comment: A cytoplasmic serine residue is phosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence of human asialoglycoprotein receptor cDNA: A;Reference number: A22509; MUID:85130911; PMID:2982798 A;Accession: A22509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A22509
R;Spiess, M.; Schwartz, A.L.; Lodish, H.F.
J. Biol. Chem. 260, 1979-1982, 1985
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A;Cross-references: GDB:118754; CMIM:108360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;60-291/Domain: extracellular #status predicted <EXT>;154-277/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;41-59/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Alternate names: asialoglycoprotein receptor H1 (ASGP-H1)
Species: Homo sapiens (man)
;Date: 31-Mar_1988 #sequence_revision 31-Mar-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-291 <SPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                         204 HIGPVNTWMGLHDQ-
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                                                                                                                                             SERTĆ--ĆPVNWVEHERŚCYWESKSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQ---H
                                                                                                                                                                                                      KGHKCSPCDTNWRYYGDSCYGFFRHNLTWBESKQYCTDMNATLLKIDNRNIVEYIKARTH
                                                                                                                                                                                                                                                                                                                   G-----IWSVMQRNYLQDENENRTGTLQQLAKRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      LVSVGPASSFWWRVMALILLILCV---
                                                                                                                                                                                                                                                              GGNVGRKMKSLESQLEKQQ-KDLSEDHSSLLLHV-KQFVSDLRSLSCQ----MAALQGNG
                                                                                                                                                                                                                                                                                                                                                                        LLSLG-----LSLLLLVVVCVIGSQNSQLQEELRGLRETFSNFTASTEAQVKGLSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YKANKTLLPSNCASKHEWIC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLHSKFNWTQERQFWIGFNRRNPLNAGSWAWSDGSPVVSSFLDNAYFEEDAK---NCAV 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCSPCDTNWRYYGD--SCYGFFRH-----NLTWEESKQYCTDMNATLLK---IDNRNIV- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CV-VVRGGSSLGRWEV-----KDCSDFK-----AMSLCKTPVKIWEKTELEERWPFH 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFHNGKMHPTFCENKHYLMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCYMDWESATGLASCFKVFHSEKVLMKRSWREAEAFCEEFGAHLASFAHIEEENFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                           ---EWVGLSRQKSNEVWKWEDGSVIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%;
22.3%;
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26.5%;
                                -NGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 138.5; DB 1
Pred. No. 7.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 139; DB 2; Length 1487;
Pred. No. 0.0004;
4; Mismatches 69; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                        -ENMFEFLEDG-KGNMNCAYF-HN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 291;
                                                                                                                                                                                                                                                                                                                   COYVVKQSELKGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                   --GMVVGLVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
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                             RESULT
I55686
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A;Map position: 12p13-12p12
C;Superfamily: C-type lectin homology
C;Keywords: glycoprotein; phosphoprotein; receptor;
F;39-64/Domain: transmembrane #status predicted <TMV
F;85-194/Domain: C-type lectin homology <LCPu
F;18,30/Binding site: phosphate (Ser) (covalent) (by
F;31/Binding site: phosphate (Thr) (covalent) (by ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: DNA
A;Rolecule type: DNA
A;Residuce: 1-199 <SAN>
A;Residuce: 1-199 <SAN>
A;Cross-references: EMBL:Z30426; NID:g525242; PIDN:CAA83017.1;
A;Cross-references: EMBL:Z30426; NID:g525242; PIDN:CAA83017.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-199 <RESS
A;Residues: 1-199 <RESS
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
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A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PIDN:AAB46359.1;
A;Cross-references: GB:L07555; NID:g291897; PI
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C;Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 08-Oct-1999
C;Accession: JH0822; I56167; $60753
R;Lopez-Cabrera, M: Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.
J. Exp. Med. 178, 537-547, 1993
A;Title: Mclecular cloning, expression, and chromosomal localization of the
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Immunol. 150, 4920-4927, 1993

A;Title: Expression cloning of the early activation antigen A;Reference number: I56167; MUID:93267093; PMID:8496594
                                                                                                                                                β,
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                                                                                                                                                                                                                                                                                                                                                                                                                           γ
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A;Gene: GDB:CD69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 860753
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;166/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S60753; MUID: 94298875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ceptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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mouse
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                                                                                                                                                                                                                                                                                                       156 IRWVGLSRQKSNEVWKWEDGSVISENWFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLM
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                                                                                                                                                                                                   CER 218
                                                                                                                                                                                                                                                           --WVGLKKEPGHP-WKWSNGKEFN-NWFNV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 137.5; DB 2;
Pred. No. 5.7e-05;
1; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (covalent) (by protein kir
ovalent) (by casein kinase
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(covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMID:8026529
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A for residue 110
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nase II)
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A;Cross-references: EMBL:X73579; NID:g313672; PIDN:CAA51981.1; PID:g313673
C;Superfamily: IgE receptor II; C-type lectin homology
C;Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; tree-relation intracellular #status predicted <INT>
F;14-25/Domain: intracellular #status predicted <INT>
F;44-46/Domain: transmembrane #status predicted <TMM>
F;47-309/Domain: extracellular #status predicted <TMM>
F;12-309/Product: soluble IgE-binding factor (25%) #status predicted <IGI>F;149-309/Product: soluble IgE-binding factor (25-27K) #status predicted <HFI>F;164-283/Domain: C-type lectin homology <LCH>
F;193-283/260-274/Disulfide bonds: #status predicted
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S34198
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A;Molecule type: mRNA
A;Residues: 1-267 <RES>
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A:Title: Cloning and functional characteristics of murine A:Reference number: IS5886; MUID:95355829; PMID:7629495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: LGL-1
C; Superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S78689; NID:g1041888; PIDN:AAC60707.1; PID:g1041889 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus sp.
C;Date: 26-Jul-1996
C;Accession: I55686
                                                                                                                                                                        Query Match
Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: I55686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gE Fc receptor II, low-affinity - rat;
Alternate names: CD23; lymphocyte IgE receptor;
Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Date: 06-Jan-1995 #sequence_revision
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;Date: 26-Jul-1996
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                          60 NYLQDE---
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                                                                                                                                                                        Conservative
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MBL Data Library, June 1993
ibition of an in vivo antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SALSEMMER-TEDGKCHANCAXEHNGKMHELECENKHATWCRKWBMIKADOTE 558
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19.5%;
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                   -NENRIGI-----LQQLAKRFCQYVVKQSELKGTFKGHKÇSFCDT
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Pred. No. 0.
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O
agkisacutacin alpha chain precursor - sharp-nosed viper N;Alternate names: fibrinogenlytic venom protein C;Bpecies: Agkistrodon acutus (sharp-nosed viper) C;Date: 04-Mar-2000 #sequence revision 04-Mar-2000 #text_cC;Accession: JC7134; pC7037 - revision 04-Mar-2000 #text_cC;Accession: JC7134; pC7037 - revision 05-35, 1999 B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu Biochem. Biophys. Res. Commun. 265, 530-535, 1999 A;Title: Purification, characterization, and cDNA cloning A;Reference number: JC7134; MUID:20025379; pMID:10558903
                                                                                                                                                                                                  RESULT
JC7134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scavenger receptor with C-type lectin type I - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_chang C;Bate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_chang C;Bate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_chang C;Bate: Molecular K; Funakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nak Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001 A;Title: Molecular cloning and functional characterization of A;Reference number: JC7595; MUID:21092718; PMID:11162630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1-39/Domain: cytosolic [amino-terminus] #status predif;16-19/Region: internalization signal YKRF F;40-56/Domain: transmembrane #status predicted <TMM>F;57-112/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:AB038518
C;Comment: This receptor, a member of the scavenger receptor family, belonging to
important role in host defense. It forms a timer and plays a role in recognizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-742 <NAK>
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JC7595
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Best Local :
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                                                                                                                                                                                                                                                                                                                        210 NKHYLMCER
                                                                                                                                                                                                                                                                                                                                                                                                157 RWVGLSRQKSNEVWKWEDG-SVISENMFEFLEDGKGN-----MNCA-YFHNGKMHPTFCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215
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                                                                                                                                                                                                                                                                                DVNNFICEK
                                                                                                                                                                                                                                                                                                                                                      -WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDFQCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       CPPHWKNFTDKCYYESVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDTNWRYYGDSCYGFFRENLTWEESKQYCTDMMATLLKIDNRNIVEYIKAR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSROKSNEVWKWEDGSVISENMFEFLEDGKGNM--NCAYFH-NGKNHPTFCENKHYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DWLHFQQKCYYFGEGSKQWIQAKFTCSDLEGRLVSIHSQKEQDFLMQHINKKE----SWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRN----IVEYIKARTHLIRWVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTLQEDLVNVKSQGLNEKRAASDSLEKLQEEVAKLWIEILMS
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Pred. No. 0.00031;
18; Mismatches 51
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predicted .
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                   new fibrinogenlytic
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versican precursor, splice form V0 - bovine N;Alternate names: chondroitin sulfate proteoglycan C;Species: Bos primigenius taurus (cattle)
                                                                              RESULT
T42389
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A;Residues: 1-1643 <SCH>
A;Residues: 1-1643 <SCH>
A;Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; FIDN:AAC24360.
A;Experimental source: brain
C;Keywords: glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1643/Product: versidan, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (cc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Experimental source: venom gland
A/Accession: PC7037
A/Molecule type: protein
A/Residues: 24-53/84-86/87-94/125-136/137-152 <CH2>
C/Superfamily: tetranectin; C-type lectin homology
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Best Local S
Matches 41
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: disulfide bond; heterodimer; venom;
Keywords: disulfide bond; heterodimer; venom;
;1-23/Domain: signal sequence #status predicted <SIG>
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,Residues: 1-152 <CHE>
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                                                                                                                                                                                                                                                                                                                              CDYGWHKFQGQCYKYFAHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRVGHDYQWIGL
                                                                                                                                                             YTCKKGTVACGOPP
                                                                                                                                                                                                                                       NDKMFEHDFRWIDGSTLQYENWRPNQPDS=FSTGEDCVVIIWHENGQWNDVPC--NYHLT
                                                                                                                                                                                                                                                                                                                                                                        CDINWRYYGDSCYGFFRHNLIWEESKQYCIDMNAILLKIDNRNIVEYIKARTHLIRWVGL
                                                                                                                                                                                                      CERKAGMTKVDQLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FV---AHLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIE--EESK---K 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAYEH -- NG--KMHPTFCENKHYLMCE 217
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Pred. No. 0.001;
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Pred. No. 5.7e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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F;2133~2154/Domain: C
F;2171-2291/Domain: C
F;2298-2354/Domain: C
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A;Title: Multiple forms of
A;Reference number: A55535
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R;Gobmalfedt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zim
J. Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of
"""" """"" precomme number: Z17954; NUID:98288320; PMID:9624174
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J. Biol. Chem. 270, 958-965,
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C;Date: 10-
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F;21-3381/Product: versican, splice form V0 #status predicted <ANT>
F;57,331,352,817,965,1017,1333,1393,1437,1483,1653,1974,2045,2074,2103,2263,2290,2356,20
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A; Residues: 1-3381 <SCH>
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A;Accession: T42389
                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                       SRQKSNEVWKWEDGSVIS-ENM----FEFLEDGKGNMNCAYFHNGKMHPTFÇENKHYLM 215
                                                                                                                        CDYGWHKFQGQCYKYFAHRRTWDAAERECRLQGAHLTSILSHEEQMFVNRVGHDYQWIGL
NDXMFEHDFRWTDGSALQYENWRPNOPDSFFSAGEDCVVIIWHENGQWNDVPC--NYHLT
                                                                                                                                                                                  CDINWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGL
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                                                                                                                                                                                                                                                   Conservative
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complement factor H repeat h
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24.6%; Fred. No. 0.0023;
77. Mismatches 70;
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55, 1995
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                                                                                                                                                                                                                                                   23;
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Pred. No. 0.0019;
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factor H rep
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A;Note: sequence extracted from NCBI backbone (NCBIP:118884)
R;Iozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; Mc
Genomics 14, 845-851, 1992
A;Title: Mapping of the versican proteoglycan gene (CSPG2) to
A;Reference number: I54179; MUID:93122792; PMID:1478664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1725,'V',1727-2405 <KRUS
A;Cross-references: GB:J02814
R;Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.; Bignami,
J. Biol. Chem. 267, 23883-23887, 1992
A;Title: Isolation of a large aggregating proteoglycan from huma:
A;Reference number: A45131; MUID:93054750; PMID:1429726
A;Contents: brain
        A;Gene: GDB:CSPG2
A;Cross-references:
                                                                   A)Cross-references: GB:S52488; NID:9263313; PIDN:AAB24878.1; PID:9263314
                                                                                                                                                                                                      A;Reference number: I54179;
A;Accession: I54179
                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 21-22,'X',24-37 <PE2>
A;Experimental source: brain
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 24-50;80-87,'D',89-119;128-155;167-218;229-259,'IR',261-268;277-283,'G',R;Krusius, T.; Gellsen, K.R.; Ruoslahti, E.
J. Biol. (Chem. 262, 13120-13125, 1987
A;Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-A;Reference number: A29348; MUID:88007514; PMID:2820964
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A;Residues: 171-210;289-303 <BIG>
A;Residues: 171-210;289-303 <BIG>
A;Residues: G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A;Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A;Reference number: A30358; MUID:89174663; PMID:2466833
                                                                                                                          A;Residues:
                                                                                                                                           A; Molecule type: DNA
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A;Residues: 208-440;1094-1385;1910-2246 <YAO>
A;Residues: 208-440;1094-1385;1910-2246 <YAO>
Brain Res. Bull. (2, 67-70, 1989)
A;Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A;Reference number: A60979; MUID:89229983; PMID:2469524
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A;Residues: 1-2409 <ZIM>
A;Cross-references: GB:X15998; NID:g37662; PIDN:CAA34128.1; PID:g37663
R;Yao, L.Y; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A;Title: Identification of the proteoglycan versican in aorta and smoot
A;Reference number: S43921; MUID:95005762; PMID:7921538
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A;Residues: 1-1479 <MUK>
A;Residues: 1-1479 <MUK>
A;Cross-references: EMBL:U56734; NID:g1336073; PID:g1336074; PIDN:AAC52729.1
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin
C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrial A;Reference number: Z22235; MUID:9635501; PMID:8702911
A;Accession: T42710
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mannose receptor, macrophage - mouse
N;Alternate rames: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision I1-Jan-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Wu, K.; Yuan, J.;
J. Biol. Chem. 271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
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F;2144-2175/Domain: EGF homology <EG2>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2309-2365/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 5q12-5q14 (C-type lectin homology; complement factor F;1-20/Domain: signal sequence #status predicted csig>F;1-249/Product: proteoglycan 24% core protein #status predicted
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FCE2_HUMAN
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V239_FOWPV
LIT2_MOUSE
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BOTA_BOTUAE
ABAL_TRIAE
PGCN_HUMAN
CVXB_CRODU

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O14594 C93427 Q92478 P10716 Q61361 P23807 P23806 P10758

PGCV_CHICK MANR_HUMAN PA2R_BOVIN PGCV_HUMAN

P22897 P49259 P06734

Q90953

mus musculu
homo sapien
gallus gall
homo sapien
composition
sos taurus

P48304 P55067

/ rattus norv

homo sapien

P81282 Q9erb4 Q62059 P13611

P70194 Q07108

homo sapien bos taurus rattus norv

mus musculu

P49260 Q60654 Q95mi4 P07306

oryctolagus mus musculu pan troglod

PAZR RABIT
KLR7_MOUSE
NKGE PANTR
LECH_HUMAN
KUCR_MOUSE
CD69_HUMAN
PGCV_BOVIN
PGCV_RAT
PGCV_MOUSE

CLFZ_HUMAN
KUCR RAT
PGCB_MOUSE
IXB_TRIFL
LITH_RAT
LITH_RAT
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LITH_HOMAN
BOTIS BOTUSA
PGCN_MOUSE
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LECZ_MERON
ABBA_TRIAB
CVAA_CRODU
PGCA_HUMAN
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CUTZ_MOUSE
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PGCA_CHICK
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P81112 trimeresuru P21855 mus musculu

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vaccinia vi crotalus at strongyloce vaccinia vi bos taurus

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CD94 MACMU

STANDARD; PRT; 179 AA.

Q9MZK9; O9GK91; Q9MZK7; Q9MZK8;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Natural killer cells antigen CD94 (NK cell relection-like receptor subfamily D, member 1).
                                                                                                                      PROSITE; PS00615; C TYPE LECTIN 1;
PROSITE; PS50041; C TYPE LECTIN 2;
Antigen; Receptor; Glycoprotein; Tr
Alternative splicing; Polymorphism.
                                                                                                                                                                                     InterPro; IPR001304; Lectin C. Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=CD94-A;
IsoId=Q9MZK9-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q9MZK9-2; Sequence=VSP 003055;
IsoId=Q9MZK9-2; Sequence=VSP 003054;
IsoId=Q9MZK9-3; Sequence=VSP 003054;
IsoId=Q9MZK9-3; Sequence=VSP 003054;
ISOId=Q9MZK9-3; Sequence=VSP 003054;
ISOId=Q9MZK9-3; Sequence=VSP 003054;
ISOId=Q9MZK9-3; Sequence=VSP 003054;
ISOID=SPECIFICITY: NATURAL KILLER CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XTAVITZ R.H., Grendell R.L., Slukvin I.I., Golos T.G.;
"Selective expression of NKG2-A and NKG2-C mRNAs and novel alternatisplicing of 5' exons in rhesus monkey decidua.";
Immunogenetics 53:69-73(2001).
-i- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
-i- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH NKG2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

MEDLINE=20322487; PubMed=10866118;

LaBonte M.L., Levy D.B., Letvin N.L.;

"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, I and D.";
                                                                                                 TRANSMEM
                                                                                                                                                                                                                                         ESSP;
                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmunogenetics 51:496-499(2000).
                                                                                                                                                                                                                                   L; AF190931; AAF74527.1; -.
L; AF190932; AAF74528.1; -.
L; AF19093; AAF74529.1; -.
L; AF294886; AAG34498.1; -.
2; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TaxID=9544;
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31
EXTRACELLULAR C-TYPE LECTIN BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.
                                                                                          SIGNAL-ANCHOR
                                                                             (POTENTIAL)
                                                                                                           CYTOPLASMIC
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                                                                                                                                     Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane protein
                                                                                                                                                                  FALSE_NEG
                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
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                                                                                          (POTENTIAL).
DR (TYPE-II MEMBRANE
                                               (POTENTIAL)
(LONG FORM)
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Best Local :
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Mammalia; E
        SEQUENCE FROM N.A., AND VARIANT THR-72.
MEDLINE=21623889; PubMed=11751968;
Shum B.P., Flodin L.R., Muir D.G., Rajalingam F
Cleland S., Guethlein L.A., Uhrberg M., Parham
                                                                                                                                            granular
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=91178434; PubMed=2007850;
Houchins J.P., Yabe T., McSherry C., Bach F.H.;
"DNA sequence analysis of NKG2, a family of related cDNA clones
encoding type II integral membrane proteins on human natural killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P26718; Q9NR41;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
NKG2-D type II integral membrane protein (N
                                                                                                                 Kothapalli R., Kusmartseva I., Loughran T.P. Jr., "Identification and characterization of the NKG2D granular Tymphocyric leukemia (LGC) cells.", Submitted (DEC-2001) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                    SEQUENCE FROM N.A. Kothapalli R., Kus
                                                                                                                                                                                                                                              "The genomic organization of NKG2C, human natural killer gene complex.", Immunogenetics 48:163-173(1998).
                                                                                                                                                                                                                                                                                                            Glienke J., Sobanov Y., Brostj
Lehrach H., Hofer E., Francis
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98350122; PubMed=9683661;
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CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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179 AA;
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Primates;
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25.3%;
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rancis F.;
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N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

MAVEXTILWRISGTIGIICLSLMATLGILLKNS ->

(in isoform 3).

/FTICLVSP 003054.
L -> LQ (In isoform 2).

/FTICLVSP 003055.

Y -> D.
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Pred.
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Catarrhini;
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No. 3e-12;
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             n R.,
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                                                                                                                                                                                                                                                                                                                       C., Nguyen
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                                 Khakoo
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PR; PT03'5; rau...

PDB; HYR; 23-MAY-01.

PDB; IKCG; 09-JAN-02.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

InterPro; IPR00235; AntifreeZeII.

DR InterPro; IPR00235; AntifreeZeII.

DR PINTS; PR00356; ANTIFREEZEII.

DR PRINTS; PR00356; ANTIFREEZEII.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS0061; C_TYPE_LECTIN_1; FALSE_NEG.

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;

KW Glycoprotein; Polymorphism; 3D-structure.

FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).
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RESULT
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VARIANT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKG2 genes.",
J. Immunol. 168:240-252(2002).
I. Immunol. 168:240-252(2002).
I. FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
I. SUBURIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
I. SUBCELIGULAR LOCATION: Type II membrane protein.
I. TISSUE SPECIFICITY: NATURAL KILLER CELLS.
                                                                                                                                                                                                                        SEQUENCE
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EMBL; AJ001687; CAA04925.1;
EMBL; AJ001688; CAA04925.1;
EMBL; AJ001689; CAA04925.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restruct use, by non-profit institutions as long as its content
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AF260135; AAF86973.1;
                                                                                                                                                                           51;
                                                                                                                                                                                      Similarity
                                                      KSNEVWKWEDGSVISENMFEFLEDGKGNMNCA-YFHNGKMHPTFCENKHYLMCERK 219
                                                                                                                                             LVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWR 107
                              PTNGSWQWEDGSILSPNLLTIIEMQKG--DCALYASSFKGYIENCSTPNTYICMQR 214
                                                                              CYKNNCYQFFDESKNWYESQASCMSQNASILKVYSKEDQDLLKLVKS
                                                                                                  YYGDSCYGFFRHNLTWEESKQYCTDMNATLLKI---DNRNIVEYIKARTHLIRWVGLSRQ
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                                                                                                                                                                                     Score 211.5; DB 1
Pred. No. 4.6e-12;
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                                                                                                                                                                          Mismatches
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NKG2-D type
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SEQUENCE
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PRINTS;
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Q9MZJ7;
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LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family
identification of novel transmembrane-deleted forms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF190943; AAF74539.1; -. InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 51:496-499 (2000).
-!- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T--!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94
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TISSUE SPECIFICITY: NATURAL KILLER CELLS.
SIMILARITY: Contains I C-type lectin family domain.
                   150
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s; PR00356; ANTIFREEZEII.
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                                                                                                                                                                                                     Similarity
                 KARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCA-YFHNGKMHPTFC
                                                   ----YS
                                                                                 TEKGHKCSPCDTNWRYYGDSCYGEFRHNLTWEESKQYCTDMNATLLKI---DNRNIVEYI
                                                                                                                    LFFCCFIAVAMGIRFIIMVTIWSAVFLNSL
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28.3%;
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Multigene family; Signal-anchor;
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Pred. No. 6.3e
38; Mismatches
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ismatches 61;
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ein (NKG2-D
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                                                                                                                                                                                                                Length 216;
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Halberg D.F., Mager R.E., Farrell D.C., Hildreth J., Quesen Loeb J.A., Holland E.C., Drickamer K.;
"Major and minor forms of the rat liver asialoglycoprotein are independent galactose-binding proteins. Primary structu glycosylation heterogeneity of minor receptor forms.";
J. Biol. Chem. 262:9828-9838(1987).
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01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE=Liver; STRAIN-Sprague-Dawley; PubMed=3234178; MEDLINE=89170119; PubMed=3234178; Sanford J.P., Elliott R.W., Doyle D.; Sanford J.P., Elliott R.W., Doyle D.;
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Eukaryota; Metazoa; Chor
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                                                                                      MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
MISCELLANEOUS: TWO TYPES OF RAT HEPATIC LECTIN HAVE BEEN
IDENTIFIED, RHL-1 AND RHL-2/3, HAVING A RELATIVE ABUNDANCE OF
RHL-2 AND RHL-3 ONLY DIFFERS IN THIR CARBOHYDRATE STRUCTURES.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type II TISSUE SPECIFICITY: EXPRESSED
                                                                                                                                                                                                                                                                                                       TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAN BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND A DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
    European
                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ev
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                                                                                                                                                                                                                                                                                        SURFACE
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Bioinformatics
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16, Last sequence update)
39, Last annotation update)
n receptor R2/3 (Hepatic lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=6319386;
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01-MAR-1992
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Calcium; i
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                           ASGR2 OR ASGR-2.
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  (Mouse).
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21, Created)
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PRT;

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receptor

(Hepatic

update) c lectin

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(MHL-2)

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pfam; PF00059; lectin_G; 1.

pfam; PF03554; lectin_N; 1.

pRINTS; PR00356; ANTIFEEZEII.

SMART; SM00034; CLECT; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00611; C_TYPE_LECTIN 1; 1.

PROSITE; PS00041; C_TYPE_LECTIN 2; 1.

Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M16347; AAA42038.1; -.
EMBL; J02762; AAA41522.1; -.
EMBL; X07636; CAA30476.1; -.
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                                                                  DQYCQMEIAHLLVINSREEQEFVVKHRGAFHIWIGLTDKDGS--WKWVDGTEYRSNEKNW
                                                                                                                                                                                                          LQKEFWTLKETLSNFSTTTLMEFKALDSHGGSRNDNLTSWETTLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal-anchor;
                                                                                                                                      DHSTLLFHLKHFPLDLRTLTCQLAFFLSNGTEC
                                                                                                                                                                                                                                                                          BEQGSHVQNLRTENPRWGGQPPSRPFPQKLCSKFRLSLLALAFNILLLVVICVVSSQSMQ
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AFTQPDNCQGHEEG-GSEDCAEILSDGLWNDNFCQQVNRWACERKRDIT
                                                                                                  KQXCTDMNATLLKIDNRNIVEY-IKARTHLIRWVGLSRQKSNSVWKWEDGSVISENWEEF
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IPR001304; Lectin C.
IPR005640; lectin N.
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153
202
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301 :
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CYTOPLASMIC (POTENTIAL)
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R -> A (IN REF. 2 AND 3).

C -> W (IN REF. 2 AND 3).
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Pred.
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No. 3
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.2e-11
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(LONG FORM)
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CARBOHYD
CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes during mammalian evolution.";
Biochim. Biophys. Acta 1087:259-261(1990).
-i- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHURATE MOISTIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGANI BIMDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED A TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND AR DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                                                                                                                                                                                                                                    PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Clectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                      SEQUENCE
                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                            Calcium;
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001304; Lectin_C.
InterPro; IPR005640; lectin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S13165; S13165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6; TISSUE=Liver; MEDLINE=91027942; PubMed=2223
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Pfam; PF03954; lectin N; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR002353;
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                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                          X53042;
                                                                                                                                                                                                                                                                                                                                                                                                                                    P06734; 1HLI.
                                                                                                         48;
                                                                                                                    Similarity
          NSREEQDFVVKHRSQFHIWIGLIDRDGS--WKWVDGTDYRSNYRNWAFTQPDNWQGHEQG
                                  DWRNIVEY-IKARTHLIRWVGLSRQKSNEVWKWEDGSVISENM-----FEFLEDG
                                                                                                                                                                                                                                                                                            Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                            CQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWESKQYCTDMNATLLKI
                                                                                                                                                    298
301
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169
170
198
271
                                                                                                        Conservative
                                                                                                                                                                            165
                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAA37211.1;
                                                                                                                                                      ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=2223888;
                                                                                                                                                                301
295
181
293
285
97
165
298
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                                                                                                                                                      34907
                                                                                                                   15.9%;
                                                                                                                                                                                                                                                                                                                                                                                                             AntifreezeII.
                                                            --NGTEC-
                                                                                                                                                                                                                                                                             Phosphorylation.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                     M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                        24;
                                                                                                  Score 200.5; UB 1,
Pred. No. 6.6e-11;
                                                                                                                                                                                   EXTRACELULAR (POTENTIAL).

EXTRACELULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N.LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IS REQUIRED
                                                                                                                                                               N-LINKED
                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                         -CPVNWVEFGGSCYWFSRDGLTWAEADQYCQLENAHLLVI
                                                                                                                                                     3A29F1AFBA68F298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane protein
EXCLUSIVELY IN H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lectin family domain.
                                                                                                                                                               (GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN HEPATIC PARENCHYMAL
                                                                                                                                                    CRC64;
                                                                                                       Indels
                                                                                                                           Length 301;
                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                               (POTENTIAL)
                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGAND
                                                                                                    Gaps
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ARE
            266
                                   189
                                                         208
RESULT
CD94_HU
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U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM Biassoni R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodriguez A., Carretero M., Glienke
Lehrach H., Francis F., Lopez-Botet
"Structure of the human CD94 C-Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein
Eur. J. Immur
          or send
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD94 HUMAN (
Q13241; O43321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98139529; PubMed=9472066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96011848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                               mmunogenetics 47:305-309(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Janier L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISSUE=Placenta;
                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
Event=Alternative_splicing;
                                                                                                                                                                                                                                             SUBCELLULAR
                                                                                                                                                                                                                                                         MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 KGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ia; Eutheria;
          an email to license@isb-sib.ch).
                     requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGEDCAEILSDGHWNDNFCQQVNRWVCEKRRNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodriguez
                                                                                                                                                                                                                                                                                                                                                                                   (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               043773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7589107;
                                                                                                                                                                                                                                                                                                                                                           (ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                  to the
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                                                                                                                                                                                                                    Named
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MEDLINE-98267245; PubMed-9601951;
Furnkawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T.
Furnkawa H., Yabe T., Yamamoto K., Juji T.;
Tohma S., Inoue T., Yamamoto K., Juji T.;
"A alternatively spliced form of the human CD94 gene.";
"A alternatively spliced form of the human CD94 gene.";
Immunogenetics 48:87-88(1998).
-i- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGN
-i- FUNCTION: PLAYS A ROLECULES BY NK CELLS AND SOME CYTOTO
CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTO
                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                            Name=3; Synonyms=CD94 alt;
Isoid=Q013241-3; Sequence=VSP 003052;
Isoid=Q013241-3; Sequence=VSP 003052;
-!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
-!- SIMILARITY; Contains 1 C-type lectin family domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1) (KP43).
KURD1 OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular characterization of human CD94: a type glycoprotein related to the C-type lectin superfar Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                                                                                                  Name=1; Synonyms=CD94-A;
IsoId=Q13241-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q13241-2; Sequence=VSP_003053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: Type II membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.;
lectin
noved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lopez-Botet
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                                                                                                                                a collaboration
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RESULT
CD94-PA
ID 94-PA
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Best Local S
Matches 48
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0006960; F:antimicrobial humoral response (sensu Inver.
GO; GO:0007166; F:cell surface receptor linked signal transdu.
InterPro; IPR001304; Lectin C.
Pfam; PF00059; lectin C.
SMART; SM00034; CLECT; 1
                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last agreence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor)
lectin-like receptor subfamily D, member 1).
                                                                                                                                                                                          CD94 PANTR
Q9MZ41;
28-FEB-2003
                                                                                                                                                                                                                                                          PANTR
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembra:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB009597; BAA24450.1; -.
EMBL; AB010084; BAA24451.1; -.
PDB; 1B6E; 15-JUN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                          Mammalia; Eutheria;
                                                                  Pan troglodytes (Chimpanzee)
                                                                                          KURD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602894;
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Y14287; CAA74663.1; JOINED.
Y14288; CAA74663.1; JOINED.
AJ000673; CAA04230.1; -.
AJ000001; CAA03845.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                              163
                                                                                                                                                                                                                                                                                                                                                                                    205
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                                                                                      OR CD94.
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UI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    و
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                              DESCEDKNRYICKQQ 177
                                                                                                                                                                                                                                                                                                                                                                                    PTFCENKHYLMCERK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSYIKARTHLIRWVGLSRQKSNBVWKWEDGSVISENMFEFLEDGKGNMNC-AYFHNGKMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPGPNIELQKDSDCCSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKG----TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWBESKQYCTDMNATLLKIDNRNI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WRLISGTLGIICLSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSB
                                                                                                                                                                                                                                                                                                                                                                                                                              LDFMSS-SQQFYWIGLSYSEEHTAWLWENGSALSQYLFPSFET-FNTKNCIAYNPNGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                      STANDARD;
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31
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                          Primates;
                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MATLGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 195.5; DB Pred. No. 1e-10; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L -> LQ (in isoform 2).
/FTId=VSP 003053.
: 1884D99E8D9583A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP_00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                          Catarrhini; Hominidae;
                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                        179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE
                                                                                                                                  (Killer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LLKNSFTKLSIEPAF
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1-1
                                                                                                                                cell
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=2162389; PubMed=11751968;
Shum B.P., Flodin L.R., Muiz D.G.,
Cleland S., Guethlein L.A., Uhrber
"Conservation and variation in humo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20350666; PubMed=10894168;
Khakoo S.I., Rajalingam R., Shum B.P.,
                                                                                                                                                            DOMAIN
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rapid evolution of NK cell receptor comparison of chimpanzees and humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muir D.G., Canavez F., Parham P.;
                                                                                                                                                                                                                                                                                                         PROSITE; PS00615; C_TYPE_LECTIN 1; FALSE_NEG PROSITE; PS50041; C_TYPE_LECTIN_2; 1. Antigen; Receptor; Glycoprotein; Transmembra:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASS I HLA-E
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF259054; AAF86964.1; -. HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE SPLICING
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                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol. 168:240-252(2002)
- FUNCTION: PLAYS A ROLE AS CLASS I HLA-E MOLECULES B
                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1; Synonyms=CD94-A;
IsoId=09MZ41-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=09MZ41-2; Sequence=VSP 003056;
IsoId=09MZ41-2; Sequence=VSP 003056;
TISSUE SPECIFICITY: NATURAL KILLER CELLS.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes."
                                                                                                                                                                                                                                                                                                                                                                                     P22897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment=Additional
              9
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                                                                                                 Similarity
LKG----TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMMATLLKIDNRNI
                                       WRLISGTLGIICLSL-
                                                              WRVMALILLILCVGYVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSE
                                                                                                                                      179
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98
61
89
152
132
                                                                                       Conservative
                                                                                                                                      ΑA;
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                                                                                                                                                              179
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                                                                                                                                      WW;
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in human and
                                                                                                                                    N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
L-> LQ (in isoform :
/FTId=VSP 003056.
W; 7244D99E8D9587E7 CI
                                                                                     Score 194.5;
Pred. No. 1.3e
37; Mismatches
                                                                                                                                                                                    EXTRACELLULAR ()
C-TYPE LECTIN ()
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA)
                                                                                                                                                                                                                                                                         CYTOPLASMIC (1
SIGNAL-ANCHOR
                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        II membrane
                                                                                                                                                                                                                                                                                                                Transmembrane; Signal-anchor; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rajalingam R.,
g M., Parham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systems.";
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liante N.M.,
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es 82;
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                                                                                                                                       CRC64;
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nier L.L.,
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Query Match
                 DISULFID
CARBOHYD
CARBOHYD
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SEQUENCE
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01-AUG-1992
01-JUN-1994
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P27471;
                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                          Hiserodt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natural killer cell surface 3.2.3).
                                                                               DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                "NKR-P1, a signal transduction Science 249:1298-1300(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=90378305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI
                                                                                                                                                     PRINTS; PR00356; ANTIFREEZBII. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                EMBL; M62891; AAA41710.1;
PIR; A35917; A35917.
HSSP; P22897; IEGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                          PROSITE; PS00615; C_TYPE_LECTIN_1; PAIPROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Antigen; Transmembrane;
                                                                                                                                                                                                                                     or send an
                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                            Giorda R.,
                                                                                                                                                                            InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION. Type II membrane protein.
TISSUE SPECIFICITY: NATURAL KILLER CELLS.
MISCELLANEOUS: LIGAND BINDING WAY BE CALCIUM DEPENDENT
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                    FUNCTION: MEDIATES TRANSMEMBRANE (NK) CELLS AND SO MAY ACT AS A RETRIGGER NK CELL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                               SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TaxID=10116;
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                  A,
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23, Last sequence update)
29, Last annotation update)
29, Tast annotation P1-3.2.3
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                       EXTRACELLULAR (
C-TYPE LECTIN (
BY SIMILARITY.
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N-LINKED (GLCNA)
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Score 187;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
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Sciurognathi; Muridae
                 N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
-LINKED (GLCNAC...
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A RECEPTOR ABLE TO SELECTIVELY
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                                                                                                                                            FALSE_NEG.
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                                                                                                                           Signal-anchor;
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                                                                               (POTENTIAL)
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Length 223;
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EMBL;
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30-MAY-2000
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M63230;
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MEDIINE=91268022; PubMed=2050668; Bezouska K., Crichlow G.V., Rose J.M., Taylor "Bvolutionary conservation of intron position encoding carbohydrate-recognition domains."; J. Biol. Chem. 266:11604-11609(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatic lectin.
Gailus gallus (Chicken).
Bukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibroblasts expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88186849;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=81215504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wellow T.E., Halberg D., Drickamer K.;
Wellow T.E., Halberg D., Drickamer Containing glycoproteins by rat
"Endocytosis of N-acetylglucosamine-containing glycoproteins by rat
                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                              SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                 non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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erg D., Drickamer K.;
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0; Mismatches 84;
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; Galliformes; Phasianidae;
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EMBL; J03188; AL..

( PIR; A03167; LNCHL.

''SSP; P20693; IHLJ.

''SSP; P20693; IHLJ.
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P26715;
01-AUG-1992 (Rel
01-AUG-1992 (Rel
15-SEP-2003 (Rel
NKG2-A/NKG2-B ty
NK receptor) (NK
KLRC1 OR NKG2A.
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EMBL;
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;
                                                                                                                                                         encoding cells.";
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                              the human
                                                  "Genomic structure, chromosome
                                                                 MEDLINE=96337918; PubMed=8753859
Plougastel B., Jones T., Trowsda
                                                                                                                                                                                             "DNA
                                                                                                                                                                                                            Houchins J.P., Yabe
                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS NKG2-A MEDLINE=91178434; PubMed=2007850;
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                       SEQUENCE
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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M63227; AAA48814.1;
M63229; AAA48814.1;
M63229; AAA48814.1;
M63229; AAA48814.1;
J03188; AAA48937.1;
                                                                                                                                                                                           hins J.P., Yabe T., McSherry C., Bach F.H., sequence analysis of NKG2, a family of rel
                                                                                                                                                                                                                                                                                     TaxID=9606;
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                NKG2A gene.";
etics 44:286-291(1996)
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-B type II integral membrane prote
) (NK cell receptor A).
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                                                                                                                                                                                                                                                                                                                                          (Human)
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 9.7e
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Catarrhini;
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EMBL; X54867; CAA38649.1; -.
EMBL; X54868; CAA38650.1; -.
EMBL; U54786; AAB17133.1; JOINED.
EMBL; U54783; AAB17133.1; JOINED.
EMBL; U54784; AAB17133.1; JOINED.
EMBL; U54784; AAB17133.1; JOINED.
EMBL; AF023840; AAQ17488.1; -.
EMBL; AF023840; AAQ17488.1; -.
EMBL; AF023850; AAAL17488.1; -.
EMBL; AF023850; AAAL17488.1; -.
EMBL; AF023850; AAL15250.1; -.
EMBL; AF02372; DF0372.
Genew; HGNC:6574; KLRC1.
MIM; 161555; -.
GO; GO:0004888; F:transmembrane rec
GO; GO:0006960; P:antimicrobial hum
GO; GO:0007166; P:cell surface rece
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Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Philippin, Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 1,000 full-length human and mouse cDNA sequences."; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).

1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF 1 CLASS I HLA-E MOLECULES BY NX CELLS AND SOME CYTOTOXIC T-CELL CLASS I HLA-E MOLECULES BY NX CELLS AND SOME CYTOTOXIC T-CELL CLASS I CAN FORM DISULFIDE-BONDED HERRODIMER WITH CD94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cluster of genes.";
Genomics 49:193-199(1998)
[4]
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE FROM N.A.
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"Sequence analysis of a 62-kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
; 161555; -.
GO:0005887; C:integral to plasma membrane; TAS.
GO:0004888; F:transmembrane receptor activity; TAS.
GO:0004860; P:antimicrobial humoral response (sensu Inver.
GO:0007166; P:cell surface receptor linked signal transdu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P26715-2; Sequence=VSP_003062;
TISSUE SPECIFICITY: NATURAL KILLER CELLS.
SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=NKG2-B;
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snmen C.M., Schuler G.D
naefer C.F., Bhat N.K.,
"and J., Hsieh F.,
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                          MEDLINE=91349596; PubMed=1880421; Giorda R., Trucco M.; Trucco M.; Trucco M.; Mouse NKR-P1. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells."; J.mmunol. 147:1701-1708(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Matural killer cell surface protein P1-34 (NKR-P1
KLRB1B OR LY55B OR LY55-3.
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                                                                           MEDLINE=92388663; PubMed=1517565;
Giorda R., Weisberg E.P., Ip T.K., Truc
"Genomic structure and strain-specific
killer cell receptor NKR-P1.";
J. Immunol. 149:1957-1963(1992).
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CYTOPLASMIC (POTENTIAL)
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Pred. No. 1.2e-08;
8; Mismatches 86;
   SIGNAL-TRANSMITTING e II membrane proteir
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PROSITE; PS50041; C_TYPE_LECTIN_2; I.
Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
DOMAIN
1 43 CYTOPLASMIC (POTENTIAL).
TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Spleen;
STRAIN=C57BL/6; PubMed=8027540;
                                                                                                             Q60653;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Killer cell lectin-like receptor 6 (T-cell su

LY-49F) (LY49-F antigen).

KIRA6 OR LY49F OR LY-49F OR LY49-F.
                                                                                                                                                                                                    KLR6
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SMART; SM00034; CLECT; 1.
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                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                      NCBI_TaxID=10090;
[1]
                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                    MOUSE
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223
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Rodentia;
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                                                                        Craniata; Vert
Sciurognathi;
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No. 2.4
                                                                                                                                                                                                    266
                                                                                        Vertebrata;
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                                                                             Murinae;
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InterPro; IPROUISUA,

If an; PRO0059; lectin c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C TYPE LECTIN 2; 1.

PROSITE; PS50041; C TYPE LECTIN 2; 1.

PROSITE; PS50041; C TYPE, LECTIN 2; 1.

T-call; Glycoprotein; Antigen; Transmembrane; Cell adhesion;

T-call anchor; Lectin, Receptor; Multigene family.

CYTOPLASMIC (POTENTIAL)

CYTOPLASMIC (TYPE-II MEMBRANE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMSI cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Ly-49 multigene family expressed by IL-2-activated NK J. Immunol. 153:1068-1079(1994).
-:- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR -:- SUBUNIT: Homodimer; disulfide-linked.
-:- SUBCELLULAR LOCATION: Type II membrane protein.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith H.R.C.,
                      Q9MZJ3; Q9MZI8; Q9MZJ1; Q9MZJ1; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat NKG2-A/NKG2-B type II integral memorane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                       MACMU
 Macaca mulatta (Rhesus macaque).
                                                                                                         NKGA
                                                                                                         MACMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
104
266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
143
171
236
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I49051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karlhofer F.M.,
                                                                                                                                                                                                      229
                                                                                                                                                                           265
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266
261
257
249
249
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (
C-TYPE LECTIN ()
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
N-LINKED (GLCNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 167.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yokoyama W.M.;
                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LINKED (GLCNAC. . .)
-LINKED (GLCNAC. . .)
AD180AA9C762F1F6 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-2-activated NK cells.";
                                                                                                         233
                                                                                                                                                                                                                                 --CVFLSKRRLEDINCKNSHYCICGX----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                         - EQNRGYSETKTDLDSSQDTGTGVKYWFCYRT
                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   i.5e-08;
ies 86;
                                       protein
                                                                                                         ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                         (NKG2-A/B activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                        ----WSVMQRNY-LQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                 260
                                                                                                                                                                                                                                                           224
                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                      111
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                                                                                                                                                                                                                                                                                      210
                                                                                                                                                                                                                                                                                                                                           152
                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                         Pfam; PF00059; lectin_G; 1.

SMARY; SM00034; CLECT; 1. FA
PROSITE; PS00615; C_TYPE_LECTIN_1; FA
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene fa
Receptor; Alternative splicing
Glycoprotein; Alternative splicing
DOMAIN

CYTOPLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS NKG2-A; MEDLINE=20322487; PubMed=10866118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                              CARBOHYD
VARSPLIC
                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                     EMBL; AF190979; AAF73835.1; --
EMBL; AF190981; AAF73837.1; --
EMBL; AF190982; AAF73838.1; --
EMBL; AF190984; AAF73840.2; --
HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9MZJ3-4; Sequence=VSP_003065;
-!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LaBonte M.L., Levy D.B., Letvin N.L.; "Characterization of rhesus monkey CD94/NKG2 family identification of novel transmembrane-deleted forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                             DISULFID
                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                TRANSMEM
                                              SEQUENCE
                                                                     VARSPLIC
                                                                                           VARSPLIC
                                                                                                                                                     CARBOHYD
                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=NKG2-Bdtm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=NKG2-Adtm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=NKG2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9MZU3-3; Sequence=VSP_003063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9MZJ3-2; Sequence=VSP_003064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9MZJ3-1; Sequence=Displayed;
 46; Conserv
                                              233
                                                                                                                              94
118
119
147
208
102
103
151
  Conservative
                                                                     63
                                                                                           96
                                              ĄΑ;
                                                                     112
                                                                                                                              233
231
130
229
229
221
102
103
151
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                                                                                                                                                                                                                                                93
                                              26286
             24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing; Named isoforms=4;
                        13.2%;
                                              MW,
  26;
                                                                                                                                                                                                  EXTRACELLULAR
C-TYPE LECTIN O
BY SIMILARITY.
  Pred. No. 5.30
6; Mismatches
                        Score 167;
                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL;
N-LINKED (GLCNAC. . . .) (POTENTIAL;
N-LINKED (GLCNAC. . . .) (POTENTIAL;
DLLSAPEKLIAGIIGIICULVLASVVTIVVIPS
                                                        Missing (\overline{\text{in}} isoform NKG2-Bdtm) /FTId=VSP_003065.
                                                                                                                                                                                                                                                SIGNAL-ANCHOR
                                                                                          Missing
                                                                                                       (in isofor
                                                                                                                                                                                                                                                            CYTOPLASMIC
                                                                                 /FTId=VSP
                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                          SIMILARITY.
                                              237B2BE36E489E76
                                                                                                                 isoform NKG2-Adtm).
                                                                                                                                                                                                                                                                                  family; Signal-anchor;
                                                                                                                                                                                                                                                                                                        FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKG2-ADTM;
                                                                                           (in isoform NKG2-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                      long as its content is in no way noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
             5.3e-08
                                                                                 003064
                        D3 1;
                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                II-EGYT)
  91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKG2-B
                       Length 233;
                                                CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECOGNITION OF MEC
CYTOTOXIC T-CELLS
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     members and of NKG2-A,
                                                                                                                                                                                                                                                MEMBRANE PROTEIN)
                                                                                                                                           (POTENTIAL).
                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND NKG2-BDTM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD94
                                                                                                                                                                                                                                                                                    Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
  26;
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 Gaps
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NKGA_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKGA PANTR
Q95MI5;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-A/NKG2-B type II integral membrane prote
NK receptor) (NK cell receptor A).
                                                                                                                                                 InterPro; IPR001304; Lectin C. Pfam; PF00059; lectin C; 1. SMART; SM00034; CLECT; 1. PROSITE: PROPERTY PROSITE: PROPERTY PROSITE: PROPERTY IN THE PROPERTY PROSITE: PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY IN THE PROPERTY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Immunol. 168:240-252(2002).

-!- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECLASS I HIA-E MOLECULES BY NK CELLS AND SOME CYCLASS I GAN FORM DISULFIDE-BONDED HETERODIMER
-!- SUBJULT: CAN FORM DISULFIDE-BONDED HETERODIMER
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21623889;
Shum B.P., Flodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q95MI5-2; Sequence=VSP_003066;
-:- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conservation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleland
  DOMAIN
                                         TRANSMEM
                                                                                                   Receptor;
                                                                                                                           PROSITE;
                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=NKG2-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=NKG2-A;
                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q95MI5-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                         PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PS50041; C_TYPE_LECTIN_2; 1.
; Transmembrane; Multigene family; Signal-anchor;
tein; Alternative splicing; Polymorphism.
CYTOPLASNIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKG2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKIYHCKHK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVMALTLITCYGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMAAILLKIDNRNIVEYIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLIAGILGIICLVLMASVVTI---VVIPSTLTQKHNNSSENTRTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARTHLIRWVGLSROKSNEVWKWEDGSVISENMFEFLEDGKGNKNCAYFHNGKMHPTFCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guethlein
                                     Bioinformatics Institute. The profit institutions as long this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KARHCGHCPEEWITYSNSCYYIGKEKRTWAESLLACTSKNSSLLSIDNEEEMKFLT
  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; PubMed=11751968;
n L.R., Muir D.G.,
hlein L.A., Uhrberg
d variation in huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r D.G., Rajalingam R.,
Uhrberg M., Parham P.
in human and common c
                 SIGNAL-ANCHOR (POTENTIAL).
    EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLICING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233
                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã
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as
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Killer cell lectin-like receptor 4 (T-cell surface LY-49D) (TY49-D antigen)
KIRA4 OR LY49D OR LY-49D OR LY49-D.
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VARIANT
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                                                                                                   STRALN=WCL, MEDLINE=20384764; cilver E.T., Gong
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                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=94300068; PubMed=8027540;
Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
"LY-49 multigene family expressed by IL-2-activated
J. Immunol. 153:1066-1079(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N
STRAIN=C57BL/6;
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    + :
                                                                                     Kane
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STRAIN=C57BL/6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammal
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                                         "Ly-49P activates NK-mediated lysis J. Immunol. 165:1771-1781(2000).
                                                                                                                                                 STRAIN=NOD,
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  FUNCTION:
SUBUNIT: F
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57BL/6; TISSUE=Spleen;
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    Homodimer;
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    RECEPTOR ON NATURAL KILLER Homodimer; disulfide-linked
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D.-E., Chang C.S.,
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PROSITE; P850041; C_TYPE_LECTIN_2; 1
T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion; Signal-anchor; Lectin; Receptor; Multigene family;
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EMBI; L78247; AAC32667.1; -.
EMBL; AF218679; AAC99592.1; -.
EMBL; AF218078; AAF99591.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q60651-1;
                  156
                                                  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q60651-2;
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                                                  QHTGRGVKVYWFCYGMKCYYFVMDRKPWSRCKQSCQNSSLTLLKIDDEDELKFLQ---
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                                                                                                                    -LKEFLKHHNNCSIMQSDINLKDELLKNKSIECNLLESLNRDQNILCDKTRTVLDYL 133
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              --RWVGLSRQKSNEVWKWEDG--SVISENMFEF-LEDGKGNMNCAYFHNGKMHPTF
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4 D
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ins 1 C-type Tectin family domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glienke J., Sobanov Y., Brostjan C.,
Lehrach H., Hofer E., Francis F.,
"The genomic organization of NXG2C, I
human natural killer gene complex.";
Immunogenetics 48:163-173(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houchins J.P., Yabe T., McSherry C. "DNA sequence analysis of NKG2, a encoding type II integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKG2-C type II integral membrane protein (NKG2-C activating receptor) (NK cell receptor C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=91178434; PubMed=2007850;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003
28-FEB-2003
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                      Genew; HGNC:6375; MIM; 602891; -.
                                                                  EMBL; X54869; CAA38651.1; -
EMBL; AJ001684; CAA04922.1;
EMBL; Y13055; CAA73498.1; -
EMBL; AF260134; AAF86972.1;
PIR; PT0374; PT0374.
                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the BW the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lymphoid;
Biassoni R.;
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FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHO CLASS I HIA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS SUBUNIT: CAN FORM DISCULFIDE-BONDED HETERODIMER WITH CD94.

SUBCELLULAR LOCATION: Type II membrane protein.

TISSUE SPECIFICITY: NATURAL KILLER CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 C-type lectin family
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Uhrberg M., Parham
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Catarrhini;
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family of related cDNA clones
proteins on human natural killer
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-C type II integral membrane protein (NKG2-C activating receptor) (NK cell receptor C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GG; GO:0004888; F:transmembrane receptor activity; TAS. GO; GO:0006568; P:cellular defense response; TAS. GO; GO:0007165; P:signal transduction; TAS. InterPro; IPR001304; Lectin_C.
                                                                   SEQUENCE FROM N.A.
MEDLINE=20322487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.
"Characterization of rhesus monkey C
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SMART; SM00034; CLECT; 1.
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                                    identification and D.";
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopith
                                                                                                                                                                                                                              KLRC2 OR NKG2C (Rhesus macaque)
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                      Immunogenetics
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                                                                                                                                                                              Cercopithecinae;
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   FUNCTION:
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22.8%;
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Pred. No. 7.9e-
32; Mismatches
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S -> F (\overline{\text{IN}} ALLELE NKG2-C*02).
/FTId=VAR_013405.
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                                                                       CD94/NKG2 family
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(IN REF. 1
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D (GLCNAC. . .) (POTENTI)

DD (GLCNAC. . .) (POTENTI)

ATLELE NKG2-C*02).
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Cercopithecidae;
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   THE RECOGNITION OF
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                                                     members and of NKG2-A,
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Q60682; 078027;
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10.NCV-1997 (Rel
16-0CT-2001 (Rel
Killer cell lect
LIY-49H) (LY49-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There is use by non-profit institutions as long as modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb-sib.ch).
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS50041; C_TYPE_LECTIN_2; Receptor; Transmembrane; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF190936; AA: HSSP; P22897; 1EGG
                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
Killer cell lectin-like receptor 8 (T-cell su
LY-49H) (LY49-H antigen).
KLRAB OR LY49H OR LY-49H OR LY49-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CDS -1- SUBCELLULAR LOCATION. Type II membrane protein. -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; Lectin_C.
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47; Conserv
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                                                                                                                                                                                                                       SKRYYCKHK 230
                                                                                                                                                                                                                                                  KHYLMCERK 219
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                                                                                                                                                                                                                                                                                                      ARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYPHNGKMHPTFCEN
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                   Rodentia;
                               Chordata;
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Pred. No. 1.5e
30; Mismatches
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BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC...
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D -> G.
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EXTRACELLULAR
                Craniata; Vert
Sciurognathi;
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. 1.5e-07;
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                                Vertebrata; Euteleostomi;
                                                                                                                                                    AA.
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                                                                                   surface
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                   Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                   glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:5
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                   Mus
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Best Local S
Matches 53
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SEQUENCE FROM N.A. (ISOFORM H1).
STRAIN-C57BL/6 X CBA; TISSU3=Lung;
STRAIN-C57BL/6 X CBA; TISSU3=Lung;
MEDLINE-95053763; PubMed=7964501;
Brennan J. Mager D. Jefferies W., Ta)
"Expression of different members of the
distinct natural killer cell subsets ar
J. Exp. Med. 180:2287-2295(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Alternatively spliced Ly-49D and activated NK cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics 44:478-482(1996).
-!- FUNCTION: RECEPTOR ON NATURAL KILLER
-!- SUBUNIT: Homodimer; disulfide-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96421544; PubMed=8824161; Silver E.T., Elliott J.F., Kane K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.,
                                                                                                                                                                          DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                           DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                       MGD; MGI:102968; KlraB.
GC; GC:0009615; P:response to
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U12889; AAA58704.1;
EMBL; L78253; AAC32668.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
T-cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed.
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                  Alternative
                                                                                                                                                                                                                                                                                          Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type II ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                  I49114; I49114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q60682-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q60682-2;
 96
                                             43
                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (Se an email to license@isb-sib.ch).
                                                                                                      Similarity
NLKEEMLTNKSIDCRPSYELLEYIKREQERWDSETKSVSDSSRDTGRGVKYWFCYGTKCY
                                                                WRVMALILLILCVGMVVGLVALGIWSVMQ-RNYLQDENENRTGTLQQLAKRFCQYVVKQS
                                             WQLIVIALGILCSLRLV-IVAVFVTKFFQYSQHKQEINE
                                                                                                                                         998
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143
171
236
236
104
                                                                                                                                                                                                                                                                               splicing
                                                                                           Conservative
                                                                                                                                                                                                                                                         45
                                                                                                                                                                                                                                                                                          Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682-2; sequence=VSP_003071; Contains 1 C-type lectin family domain.
                                                                                                                                         AA;
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261
257
249
249
104
41
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                                                                                                                                         31393
                                                                                                      12.7%;
21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                          Μ.
                                                                                          41;
                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT
                                                                                                      Score
Pred.
                                                                                                                                       Missing (in isoform /FTId=VSP 003071. 3CB5A8EFZEB401E2 C
                                                                                                                                                                                                                                                          CYTOPLASMIC (I
SIGNAL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                            viruses;
                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                           Mismatches
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the Ly-49
s and cell
                                                                                                      160.5;
No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NK)
                                                                                                      ); DB 1;
                                                                                                                                                                                                                                                          (POTENTIAL).
DR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                             family;
                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene family defines adhesion properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELLS
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                                                                                                                                          CRC64;
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                                                                                                                 Length
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                                               -HILLI-
                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASS
                                                                                                                   266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
                                                RHNCSNMQRDF
                                                                                             77;
                        -WRYYGDSCY
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01~FEB-1996
01~FEB-1996
28-FEB-2003
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RAT
MMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ti M., Kurata H., Itoh N., Identification of the Molecular cloning and sequence analysis macrophage lectin specific for galactose rainl. Chem. 265:11295-11298 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 3, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Macrophage asialoglycoprotein-binding protein (M-ASGP-BF)
galactose/N-acetylgalactosamine-specific lectin) (MMGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88339956;
Ii M., Kawasaki T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGL1 OR MGL.
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                binding protein.",
Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                         galactose/N-acetylgalactosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
            DOMAIN
DOMAIN
                                                                                                               Pfam; PF00059; lectin_c; 1. Pfam; PF03954; lectin_N; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                           EMBL; J05495; AAA41216.1;
PIR; A42230; A42230.
                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY SEQUENCE OF 9-28.
MEDLINE=88339956; PubMed=3421964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90293078;
 DISULFID
                                                              Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural similarity between the macrophage
                                                                                                                                                   InterPro; IPR001304; Lectin_C.
InterPro; IPR005640; lectin_N.
                                                                                                                                                                               HSSP; P06734; 1HLI.
                                                                                        PROSITE;
                                                                                                    PROSITE;
                                                    PRANSMEM
                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMO-OLIGOMER
                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type II membrane protein SIMILARITY: Contains 1 C-type lectin family do
                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260
                                                                          Glycoprotein;
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                                                                                     PS00615; C TYPE LECTIN 1; 1. PS50041; C TYPE LECTIN 2; 1.
 59
174
175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2358462;
                                                                                                                                                                                                                                                                                                                                                                                                  Res.
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Rodentia;
 306
300
186
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                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                  Commun.
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(POTENTIAL)
EXTRACELLULAR
C-TYPE LECTIN
BY SIMILARITY.
                                                  CYTOPLASMIC (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Ver
Sciurognathi;
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NAL GALACTOSE AND
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                                                                 Calcium; Signal-anchor.
                                                                                                                                                                                                                                              (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                          phage lectin specific for hepatic asialoglycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawasaki T.; of cDNA encoding the and N-acetylgalactosamine.";
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                                                     (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAYFHNGKMHPTFCENKHYLMCERK
                 (LONG FORM)
                                                                                                                                                                                                                                                       Usage,
                                                                                                                                                                                                                                                                                                                                     domain.
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                                                      MEMBRANE
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RESULT
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Best Local S
Matches 41
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DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 20
_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLR3_MOUSE STANDARD; PRT; 266 AA Q64329; Q61154; Q64257; Created)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Killer cell lectin-like receptor 3 (T-cell LY-49C) (LY49-C antigen) (Lymphocyte antigen)
TLR43 OR LY49C OR LY-49C.
Wong S., F
Submitted
[6]
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6 X CBA; TISSUE-Lung;
MEDLINE-3132459; PubMed=1869832;
MEDLINE-3132459; PubMed=1869832;
Wong S., Freeman J.D., Kelleher C., Mager D., Takei F.
"Ly-49 multigene family. New members of a superfamily
membrane proteins with lectin-like domains.";
J. Immunol. 147:1417-1423(1991);
                                                                                                                                                                                                                                                                                                                                   MEDLINE-95355830; PubMed=7629496; Stoneman E.R., Sennett M., An J., Chesnut K.A., Wakeland Scheerer J.B., Siciliano M.J., Kumar V., Mathew P.A.; "Cloning and characterization of SE6(Ly-49C), a receptor expressed on a subset of murine natural killer cells."; J. Exp. Med. 182:305-313(1995).
                                                                                                                                               MEDIJNE=95356819, PubMed=7630404,
Held W. Roland J. Railet D.H.;
"Allalic exclusion of Ly49-family
receptors on NK cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                        STRAIN=C57BL/6 X CBA; TISSUE=Lung; Wong S., Freeman J.D., Kelleher C.,
                                                                         STRAIN=A/SN;
Sundback J., Karre K
Submitted (MAY-1996)
                                                                                                                                                                                                   STRAIN=C57BL/6,
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CB.17;
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o the EMBL/GenBank/DDBJ
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             her C., Mager D.,
EMBL/GenBank/DDBJ
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Pred. No. 2.8
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                                                                                    C.L.;
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EMBL; U09739; AAAA66973.1; -.
EMBL; U49865; AAA92252.1; -.
EMBL; U49866; AAA92253.1; -.
EMBL; U49867; AAA92253.1; -.
EMBL; U49868; AAA92554.1; -.
EMBL; U49868; AAA19253.1; -.
EMBL; U10305; AAA19253.1; -.
EMBL; U10305; AAA19101.1; -.
EMBL; U36405; AAB19101.1; -.
EMBL; U34892; AAC177066.1; -.
EMBL; U34892; AAC17703.1; -.
EMBL; U34892; AAC17703.1; -.
EMBL; U34892; AAC17703.1; -.
EMBL; U34892; AAC17703.1; -.
EMBL; U34892; AAC1703.1; -.
EMBL; U49863; I49363.
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                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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CARBOHYD
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                                                                        NZB, 129/SVJ AND COULT
T -> I (IN STRAINS BALB/C X CE
129/SVJ AND CS7BL/6).
AV -> TI (IN STRAINS BALB/C X
NZB, 129/SVJ AND CS7BL/6).
N -> S_(IN STRAINS BALB/C X CE
                                  129/SVJ AND C57BL/6).
H -> Y (IN STRAINS BA
129/SVJ AND C57BL/6).
S -> R (IN NZB AND 12
T -> L (IN STRAINS BA
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         AND C57BL/6)
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129/SVJ AND C57BL/6).
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         STRAIN 129/SVJ)
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p49300;
01-FEB-1996 (Rel. 33, Created)
01-FEB-296 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Macrophage asialoglycoprotein-binding protein 1 (M-ASGP-BP)
(Macrophage galactose/N-acetylgalactosamine-specific lectin)
MGL1 OR MGL.
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                  SEQUENCE FROM N.A. STRAIN=C3H/HeN;
                                                    Mus musculus (Mouse)
Bukaryota; Metazoa;
Mammalia; Eutheria;
                                              NCBI_TaxID=10090;
         MEDLINE=92268032;
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  Ξ.
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Rodentia;
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K -> E (IN STRAINS E 129/SVJ AND C57BL/6)
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P -> Q (IN S'
AND C57BL/6)
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Pred. No. 4.4e-07;
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I -> T (IN STRAINS E
129/SVJ AND C57BL/6)
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F -> Y (IN STRAINS BA
129/SVJ AND C57BL/6).
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Sciurognathi;
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> N (IN STRAIN NZB).
> I (IN STRAIN NZB).
> H (IN STRAINS BALB/C X
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InterPro; IPR001304; Lectin C.
InterPro; IPR005640; Lectin N.
Pfam; P700059; lectin C; 1.
Pfam; P700059; lectin C; 1.
Pfam; PF03954; lectin N; 1.
PAINTS; PR00356; ANTIFREEZEII.
SMART; SN00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Purification and characterization of a lectin-like molecule for galactose/N-acetyl-galactosamine from tumoricidal macroph J. Blochem. 104:607-605 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macrophages.";
J. Biochem. 111:331-336(1992)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S36676; AAB22171.1; PIR; JX0209; JX0209.
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PROSITE; PS50041; C
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MGD; MGI:96975; MG
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                                                                                  TLDNTTSKIKAEFQSLDSRADSFEKGISSLKVDVEDHRQELQAGRDLSQKVTSLESTVEK
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           RHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKAR
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MEDLINE=92013158; PubMed=1680927;
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28-FEB-2003 (Rel. 41, Last annotation update)
Natural killer cell surface protein P1-2 (NKR
KLRBIA OR LY55A OR LY55.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M77676; AAA39822.1; EMBL; M77753; AAA39366.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mouse NKR-P1. A family of genes selectively lymphokine-activated killer cells.";
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                                                                                                                                                                                                                                                                         SMART;
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InterPro; IPR001304; Lectin_C.
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                                                                                                                                                                                                                                                                    PF00059; lectin_c; l.
S; PR00356; ANTIFREEZEII.
; SM00034; CLECT; l.
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email to license@isb-sib.ch)
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CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II MEMBRANE
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EXTRACELLULAR
C-TYPE LECTIN
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N-LINKED (GLCN/
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ziegler S.F., Ramsdell F., H. Grabstein K.H., Hennen K.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93314711; PubM
Ziegler S.F., Ramsdell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type II membrane protein.
TISSUE SPECIFICITY: EXPRESSED ON TEE SURRACE OF ACTIVATED
B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.
B-CELLS, NATURAL STAGE: BARLIEST INDUCIBLE CELL SURFACE GLYCC
ACQUIRED DURING LYMPHOLD ACTIVATION
ACQUIRED DURING LYMPHOLD ACTIVATION OF T LYMPHOCYTES.
PIN: CONSTITUTIVE SER/THE PHOSPHORYLATION IN BOTH MATURE
THYMOCYTES AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                       ; L23638; -; NOT_ANNOTATED MGI:88343; Cd69.
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                                                                                non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
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redell F., Hjerrild K.A.,
Farrah T., F
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anslow W.C., (
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                                                                                                                         Usage,
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| T 01-NOV-1997 (Rel. 35, Last sequence update) |
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM NKG2-E).
MEDLINE=94102823; PubMed=8276448;
Adamkiewicz T.V., McSherry C., Bach F.H., F
"Natural killer lectin-like receptors have
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        SEQUENCE FROM N.A.
                                                                                                                                               Glienke J., Sobanov Y., Brost;
Lehrach H., Hofer E., Francis
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                                                        genomic organization of NKG2C, n natural killer gene complex."; nogenetics 48:163-173(1998).
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Lopez-Bottet M., Aparicio P.;
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aggregation of an activatory CD94/kp39
J. Immunol. 162:3996-4002(1999).
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SMART; SM00034; CLECI I. ECTIN 1; FALSE_MEGG.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Receptor; Transmembrane; Multigene family; Signal-anchor; Receptor; Transmembrane; Multigene family; Signal-anchor; Receptor; Transmembrane; Multigene family; Signal-anchor; Receptor; Transmembrane; Polymorphism.

Transmembrane; Multigene family; Signal-anchor; Receptor; Transmembrane; Polymorphism.

Transmembrane; Multigene family; Signal-anchor; Receptor; Transmembrane; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004888; F:transmembrane
GO; GO:0006968; P:cellular defen
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                                               SEQUENCE
                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q07444-2; Sequence=VS2_003067; TISSUE SPECIFICITY: NATURAL KILLER CELLS
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                                                                                                                                 NRNDIMIA (in isoform NKG2-H).
/FTId=VSP_003067.
P -> R (IN ALLELE NKG2-E*02).
                                                                                                                                                                                                                           N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR
C-TYPE LECTIN
    Score
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RRGFIMLTRLVLNS -> VSISFRIKALELAVHQIKFYICS
                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                    /FTId=VAR 013296.
R -> S (IN dbSNP:1138437)
/FTId=VAR_014660.
                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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                                                   20691FBZ1274D8A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor activity;
ase response; TAS.
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Q60652;
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                                                                                                                                                                                            InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS
-!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- SIMILARITY: Contains 1 C-type lectin family dom
                                                                                                                                                                                                                                                                                                                                                                                                              Smith H.R.C., Karlhofer F.M., Yokoyama W.M.; "Ly-49 multigene family expressed by IL-2-activated J. Immunol. 153:1068-1079(1994).
                                                                                                                                      Signal-anchor;
                                                                                                                                                                                                                            MGD; MGI:101903; Klra5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
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Killer cell
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                                                                                                      DOMAIN
                                                                                                                            TRANSMEM
                                                                                                                                                             T-cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                    ; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Antigen; Transmembrane; Cell adhesion; anchor; Lectin; Receptor; Multigene family.
anchor; Lectin; Receptor; Multigene family.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pell lectin-like receptor (LY49-E antigen).
                                                                                                                                                                                                                                                                          non-profit institutions as lon and this statement is not remove requires a license agreement (S an email to license@isb-sib.ch).
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                                                     EXTRACELLULAR
C-TYPE LECTIN
BY SIMILARITY.
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N-LINKED (GLCN)
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6; Mismatches
                                                                                                                         SIGNAL-ANCHOR (TYPE-II
 Score 151.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
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smatches 73;
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(GLCNAC...)
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        Padlan E.A., Helm B.A.;

Modeling of the lectin-homology de
affinity Fc epsilon receptor (Fc ep
affinity Fc epsilon receptor HAS ESS
-!- FUNCTION: THIS ESCEPTOR HAS ESS
IGE PRODUCTION AND IN THE DIFF
CELL-SECIFIC ANTIGEN)
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MOUSE
FCE2_N
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"Isolation, c...
"onlike Fo r
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for IgE (Fc
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01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Low affinity immunoglobulin epsilon FC receptor receptor) (FC-epsilon-RII) (CD23).
                                                                                                                                                                                                                                                   Gollnick S.O., Moore K.W.;
                                                                                         MEDLINE=94191542;
                                                                                                                                                           Kondo H.,
                                                                                                                                                                  STRAIN=DBA/2;
MEDLINE=94372613; PubMed=8086828;
                                                                                                                                                                                                                                                                          MEDLINE=90171598; PubMed=2137845;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       affinity receptor
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MEDLINE=90017519;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor) (FC-e
FCER2 OR FCER2A
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                                                                                         3D-STRUCTURE MODELING OF LECTIN D
MEDLINE=94191542; PubMed=8142907;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Proc. Natl.
                                                                                                                                                                                                                                                                                                                                            Conrad
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                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                  "Molecular structure
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  SUBCELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                                        f cDNAs for new subtypes
c epsilon RII/CD23).";
Allergy Immunol. 105:38-
                                                                                                                                                            Ichikawa
                                                                                                                                                                                                                 characterization, a c receptor for IgE ( 144:1974-1982(1990)
                                                                                                                                                                                                                                                                                                                                                      17519; PubMed=2529542; Hofstetter H., Rao M.,
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. U.S.A. 86:7566-7570(1989)
                                                                                                                                                           Nakamura K
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Туре
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8; Mismatches 94;
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InterPro; IPR001304; Lectin C.
Pfam; PF00059; lectin C.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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EMBL; M34163; CAA45530.1; --
EMBL; X64223; CAA45533.1; --
EMBL; X64224; CAA45533.1; --
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PROSITE; PS50041; C_TYPE_LECTIN 2; 1.

IGB-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell; Repeat; Lectin; Signal-anchor; Alternative splicing; 3D-structure.

Repeat; Lectin; Signal-anchor; Alternative (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

TRANSMEM 24 49 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
MISCELLANBOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES AND MONOCOTTES.
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Event=Alternative
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MGI:95497; Fcer2
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native splicing;
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MEENEYS -> MDTHHT
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-BUG-1992 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Natural killer cell surface protein P1-40 (NXR-P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                MEDLINE-92373004; PubMed=1506685;
Ryan J.C., Turck J., Niemi E.C., Yokoyama W.M., Sear Ryan J.C., Turck J., Niemi E.C., Yokoyama W.M., Sear Payan J.C., Turck J., Niemi E.C., Yokoyama W.M., Sear Payan J., Immunol Adming of the NKI.1 antigen, a member of family of natural killer cell activation molecules. J. Immunol 149:1631-1635(1992)
J. Immunol 149:1631-1635(1992)
J. Immunol 149:1631-1635(1992)
J. TURCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RISUBCELLULAR LOCATION: Type I membrane protein.
J. TISSUE SPECIFICITY: NATURAL KILLER CELLS.
J. SIMILARITY: Contains 1 C-type lectin family dom.
                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             Giorda R., Trucco M.;
"Mouse NKR-Pl. A family of genes selectively coexpressed in adherent
lymphokhire-activated killer cells.";
J. Immunol. 147:1701-1738(1991).
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SEQUENCE FROM N.A
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                SWISS-2DPAGE; P27814; M
MGD; MGI:107538; Klrblc
                                          EMBL; M77678; AAA39824.1; PIR; C46467; C46467.
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Best Local S
Matches 44
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DOMAIN
DISULFID
DISULFID
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
          MEDLINE=89140367; PubMed=278394
Chan P.-Y., Takei F.;
"Molecular cloning and characte
surface antigen, YE1/48";
J. Immunol. 142:1727-1736(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen)
KLRA1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LY4A MOU
P20937;
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                                                                                                                                "A murine T lymphocyte antigen belongs II integral membrane proteins.";
J. Immunol. 143:1379-1386 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein YEI/48 (T lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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                                                                                                                                                                                                                                         MEDLINE=89309828; PubMed=2787364;
Yokoyama W.M., Jacobs L., Kanagaw
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE
                                                                 ALLELES. INHIBITS THE CELL LYSIS.
     SUBUNIT: Homodimer; di
SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: HI
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; SM00034; CLECT; 1.
TE; PS00615; C_TYPE_LECTIN_1; FAI
TE; PS00041; C_TYPE_LECTIN_2; 1.
pprotein; Antigen; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199
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                                                                                                                                                                                                                                                                                             FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220
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F.;
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22.9%;
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     HIGH,
                                                         disulfide-linked
                                                                                                          NATURAL F
                                                                                                                                                                                                                                         Kanagawa O.,
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(POTENTIAL).

EXTRACELLULAR (POTENTIAL).

C-TYPE LECTIN (LONG)

BY SIMILARITY.

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; Mismatches
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Pred. No. 1.
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
NITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
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     I membrane property of the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second sec
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to a supergene
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; Murinae; Mus
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PREVENTING
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e family
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RESULT 29
LECH_MOUSE STAN
1D LECH_MOUSE STAN
AC P34927; Q64363;
DT 01-FEB-1994 (Rel. 2
DT 15-JUL-1998 (Rel. 3
DT 30-MAY-2000 (Rel. 3
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MGD; MGI:101907; Klra1.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; P700059; lectin_c; 1.

SMART; SM00034; CLECT; 1. FALSE_NEG
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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PIR; A45813; A45813.
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EMBL; M25812; AAA37242.1; -.
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SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                                                 Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Antigen; Transmembrane; Cell adhesion; anchor; Lectin; Receptor; Multigene family; 3D-structure.

1 44 CYTOPLASMIC (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                           11.9%;
21.5%;
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 Last sequence update)
Last annotation update)
                         Created)
                                                                                                                                                                                                                                                                                                                                                                                               MW;
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BY SIMILARITY.
BY SIMILARITY.
CELL ATTACHMENT SITE.
N-LINKED (GLCNAC. . .) (POI
N-LINKED (GLCNAC. . .) (POI
N-LINKED (GLCNAC. . .) (POI
N-LINKED (GLCNAC. . .) (POI
NCE -> KLQ (IN REF. 2).
I -> M (IN REF. 2).
A -> T (IN REF. 2).
A -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                Score 149.5; DB 1;
Pred. No. 2.3e-06;
6; Mismatches 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                  283
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(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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                                                                                                                                                                                                                                                                           -TNWRYYGDSCYG
                                                                                                                                                                                                                                                                                                                                                 59;
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ctions on its
in no way
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7 4 1

-NGPWKWVDGT

280 226 225 176 20;

Gaps

6

167

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EMBL; D13517;
EMBL; U09362;
EMBL; U08372;
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=904774..., Monroe R.S., Huber B.E.;
"The major form of the murine asialoglycoprotein receptor:
"The major form of the murine asialoglycoprotein receptor:
"The major form of the murine asialoglycoprotein receptor:
              DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence and expression in liver, Gene 148:237-244(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Determination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takezawa R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asialoglycoprotein receptor 1 (Hepatic lectin 1) (MEL-1) (ASGP-R) (ASGPR)
                                                                                                                                                    Calcium;
INIT MET
                                                                                                                                                                                                                                                                                                      MGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93176818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGR1 OR ASGR-1.
                                                                                                                                                                           PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Receptor; Endocytosis;
                                                                                                                                                                                                              Pfam; PF00059; lectin c; 1.
Pfam; PF03954; lectin N; 1.
PRINUS; PR00356; ANTIFEEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                             InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin C.
InterPro; IPR005640; lectin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---
                                                   DISULFID
                                                             DISULFID
                                                                                      DOMAIN
                                                                                                     DOMAIN
  CARBOHYD
                                                                                                                                        DOMAIN
                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARSOHYDRATE MOIETLES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISASSOCIATED.
                                                                                                                                                                                                                                                                                                     MGI:88081; Asgr1.
                                                                                                                                                                                                                                                                                                                   P20693; 1HLJ
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                                                                                                                                                               Signal-anchor;
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180
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و
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                                                                                                                                                                                                                                                                                                                                          BAA02734.1; -. AAB60441.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contains 1 C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8439566;
zawa K., Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=7958950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse major asialoglycoprotein
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BY SIMILARI
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EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
ENDOCYTOSIS SIGNAL (POTENTIAL
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BY SIMILARITY.
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                                                                                                               CYTOPLASMIC (POSIGNAL-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akaike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family domain.
                                                                                                                           (POTENTIAL)
DR (TYPE-II
                                                                                                                                                                             Transmembrane;
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                                                                            (POTENTIAL)
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  (POTENTIAL)
(POTENTIAL)
                                                                                                                            MEMBRANE
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RHCA_AGKRH
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SEQUENCE
                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viperidae; Crotalinae; Calloselasma.
NCBI_TaxID=8717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Cre
15-JUL-1998 (Rel. 36, Las
28-FEB-2003 (Rel. 41, Las
Rhodocetin alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHCA
                                                                                                                              Lectin.
                                                                                                                                                    Pfam; PF00059; lectin_c;
SMART; SM00034; CLECT; 1
PROSITE; PS00615; C_TYPE
PROSITE; PS50041; C_TYPE
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99303998; PubMed=10360956;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P81397;
                                                                                                                                                                                                                  HSSP; P23806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sepidosauria; Squamata; Scleroglossa;
                                                                                                                                                                                                      [nterPro;
                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
MASS SPECTROMETRY: WM=15955.90;
SIMILARITY: Contains 1 C-type 1
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                                                                                                                                                                                                                                                                   disulfide bridges.
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                            42;
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                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             Kini R.M.,
     CDTNWRYYGDSCYGFFRHNLTWEESKQYCTDM--NATLLKIDNR--
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION,
                                                                                                                                                                                                      IPR001304; Lectin_C.
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                              Conservative
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                                                                                                                                                   C_TYPE_LECTIN_1;
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24.3%;
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                                                                                        C-TYPE LECTIN
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3; Mismatches
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                              Pred. No. 1.30
L; Mismatches
                                                    Score
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                                                                              386EAC519DFC674D
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MASS
                                                                                                                                                                                                                               ); MW_ERR=1.44; METHOD=Electrospray lectin family domain.
                                        148.5;
No. 1.3
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, 2.8e-06;
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                                                       DB 1;
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RESULT 31

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-1693(2002).

CC WHICH THE TERMINAL SIALIC ACID RESIDUS ON THEIR RECEPTOR RECCONTIES TO COMPLEX IS INTERNALIZED AND TRANSPORTED TO A SORTING ORGANIELLE, WHERE RECEPTOR RAD LIGAND ARE TRANSPORTED TO A SORTING ORGANIELLE, WHERE RECEPTOR AND LIGAND ARE TRANSPORTED TO A SORTING ORGANIELLE, WHERE RECEPTOR AND LIGAND ARE TRANSPORTED TO A SORTING ORGANIELLE, WHERE RECEPTOR AND LIGAND ARE
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LECI HUMAN STANDARD; PRT; 311 ....
P07307; 000448; Q03969;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Differences in the abundance of variably spliced transcripts for second asialoglycoprotein receptor polypeptide, H2, in normal and transformed human liver.";
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Mammalia; Eutheria; Primates;
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oc. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).
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      DISASSOCIATED. SURFACE.
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GO; GO:0004873; F:asialoglycoprotein receptor activity; TAS.
GO; GQ:0007166; P:cell surface receptor linked signal transdu.
InterPro; IPR001304; Lectin_C.
InterPro; IPR005640; lectin_N.
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PIR; A25179; LNHU2A.
HSSP; P06734; 1HLI.
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EMBL; U97197; AAB58308.1; -.
EMBL; X55283; CAA38997.1; -.
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TISSUE SPECIFICITY:
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                                                                                                                                                          40;
                                                                                                                                                                           Similarity
SWEEQKFIVQHTNPFNTWIGLT--DSDGSWKWVDGTDYRHNYKNWAVTQPDNWHGHELGG
                                     NRNIVEYIKARTHLIR-WVGLSRQKSNEVWKWEDGSVISENMFEFL---
                                                                         REVACOMELLHS-NGSORTCCPVNWVEHQGSCYWESHSGKAWAEAEKYCQLENAHLVVIN
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                                                                                                                                                                                                                                                                                                                  <u>د</u>ا
.
                                     -EDGKG
                                                                                                                                                      Gaps
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RESULT 32
LECH_RAT
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P02706;
                                                                                                                                                                                                                                                                                                                               asialoglycopxotein receptor.",

Blosci. Rep. 6:527-534(1986).

-i-FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLCALLACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AN TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL. The European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation updat
                                                                     PIR;
                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holland E.C., Leung J.O., Drickamer K.; "Rat liver asialoglycóprotein receptor lacks a cleavable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=85063786; PubMed=6095287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asialoglycoprotein receptor.";
J. Biol. Chem. 260:12523-12527(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of the gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mamma⊥la;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watts C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87026895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASGR1 OR ASGR-1
                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and expression of cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ASGPR)
                                         InterPro;
                                                                                                                                                                                                                         MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
MISCELLANEOUS: TWO TYPES OF RATHEPATIC LECTIN HAVE BEEN
IDENTIFIED, RHL-1 AND RHL-2/3, HAVING A RELATIVE ABUNDAN
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: CELLS.
                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type II TISSUE SPECIFICITY: EXPRESSED
                                                                                                                                                                                                                                                                                                                       SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192
                                                                   A92497; LNRTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275
                                                                                K02817; AAA42037.1;
M21770; AAA40764.1;
                                                        P20693; 1HLJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEDCVEVOPDGRWNDDFCLOVYRWVCEKRRNAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NMNCAYFH-NGKMHPTFCENKHYLMCERKAGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 11-283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                IPR001304;
IPR005640;
                                          IPR002353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08335; PubMed=2995379;
Holland E.C., Drickamer K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  lectin_c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 FROM N.A.
PubMed=2945599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
               Lectin_C.
lectin_N.
                                          AntifreezeII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81:7338-7342(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                           membrane protein.
EXCLUSIVELY IN HEPATIC PARENCHYMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
c lectin
                                                                                                                                  noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                          There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                      for a rat liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tebrata; Euteleostomi;
Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rat liver
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                                                                                                                                                                                                                                         ABUNDANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NH2-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASGP-R
                                                                                                                                               d for
                                                                                                                                                                                                 a collaboration
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                                                                                                                                                                                      outstation
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no
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KLR2_MOUSE
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                    16-OCT-2001
Killer cell
LY-49B) (LY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
Lectin, Glycoprotein; Receptor; Endocytosis;
Calcium; Signal-anchor; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                Mammalia; Eutheria;
NCSI_TaxID=10090;
                                                                                                                                                                                                                                                                                           LY-49B) (LY49-B antigen).
KLRA2 OR LY49B OR LY49-B.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                     KLR2 MOUSE
Q60660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                      - -
                                                                                                                                              Wong S., Freeman J.D., Kelleber C., Mager I "Ly-49 multigene family. New members of a smembrane proteeins with lectin-like domains J. Immunol. 147:1417-1423(1991).
                                                                                                                                                                                                 STRAIN=C57BL/6 X CBA; TISSUE=Lung; MEDLINE=91332459; PubMed=1869832;
                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA;
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                           FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR SUBUNIT: Homodimer; disulfide-linked. SUBCELLULAR LOCATION: Type II membrane protein. SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF03954; lectin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMFEFLEDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGFKNWRPGQPDDWYGHGLGGGEDCAHFTTDGHWNDDVCRRPYRWVCETELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PWTBADKYCQLENAHLVVVTSWEEQRFVQQHMGPLNTWIGLTDQ--NGPWKWVDGTDY-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWEESKOYCTDWNATLLKIDNRNIVEYIKART-HLIRWVGLSROKSNEVWKWEDGSVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LREDHSRLLLHVKQLVSDVRSLSCQMAALRGNGSERIC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQDENENRIGILQQLAKRFCQYVVKQSELKGTFKGHKCSFCDINWRYYGDSCYGFFRHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
283
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151
152
152
180
253
74
77
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
lectin-like receptor 2 (T-cell su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283
277
163
2675
2675
2774
27718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 9
9 8
                                                                                                                                                                                                                                                                  Ročentia;
                                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 145.5; UB 1, pred. No. 5.7e-06; 82;
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N-LINKED (GLCNAC. ..) (
N-LINKED (GLCNAC. ..) (
N-LINKED (GLCNAC. ..) (
O -> R (IN REF. 2).

G -> R (IN REF. 2).
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BY SIMILARITY.
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ENDOCYTOSIS SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNMNCAY - HNGKMHPTFCENKHYLMCERKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                  Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                    D., Takei F.; superfamily of type
                                                                                                                                                                                                                                                                                                                                   surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                                                                  glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                    FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                 Murinae; Mus
                                                                                                                                    CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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180 171 121 σ

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PA2R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                       "Cloning and expression of a membrane receptor for phospholipases A2.";
J. Biol. Chem. 269:1575-1578/100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                           P49260;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
T-cell; Glycoprotein; Antigen; Transmembrane; Cell
Signal-anchor; Lectin; Receptor; Multigene family.
DOMAIN
1 45
CYTOPLASMIC (POTENTIAL
TRANSMEM 46 66
SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                 180 kDa secretory phospholipase A2 receptor precursor Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euthandata; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                     -!- SUBCELLULAR LOCATION-!- TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                PA2R_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:101906; Klra2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL
                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin_C.
                                                                                     Biol. Chem. 269:1575-1578(1994).
FUNCTION: MAY HAVE A KEY ROLE I
OF SECRETORY PHOSPHOLIPASE A2.
   HEART.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I49058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 WRVMALILLILC--VGMVVGLVALGIWSVMQRNYLQDENENRTGTLQQLAKRFCQYVVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
49; Conser
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21.0%;
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Pfam; P700059; lectin c; 8.

Pfam; P700059; rictin B lectin; 1.

ProDom; P0000995; rN Type_II; 1.

SMART; SM00034; CLECT; 8.

SMART; SM00059; FN2; 1.

SMART; SM00059; FN2; 1.
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PROSITE; PSO041; C_TYPE LECTIN_2; 8.

PROSITE; PSO043; FIRCOMECTIN_2; 1.

PROSITE; PSO023; FIRCOMECTIN; 1.

PROSITE; PSO0231; RICIN_B_LECTIN; 1.

PROSITE; PSO0231; RICIN_B_LECTIN; 1.

Signal; Receptor; Transmembrane; Repeat; Glycoprotein; Lectin.

SIGNAL 1 23 PROVIDEL.

CHAIN 24 1458 180 kba SECRETORY PHOSPHOLIPASE A:
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InterPro; IPR001304; Lectin C
InterPro; IPR000772; Ricin_B_lectin.
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HSSP; P02751; 2FN2.
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brennan J., Mager D., Jefferies W., Takei "Expression of different members of the I distinct natural killer cell subsets and J. Exp. Med. 180:2287-2295(1994).
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a contween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94300068; PubMed=8027540;
Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
"LY-49 multigene family expressed by IL-2-activated
J. Immunol. 153:1068-1079(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                   Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

T-cell; Glycoprotein; Antigen; Transmembrane; Cell
Signal-anchor; Lectin; Receptor; Multigene family;
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                                                                                                                                                                                                      EMBL; U10093; AAA50221.1;
EMBL; U10094; AAA50222.1;
EMBL; U10095; AAA50223.1;
EMBL; U12890; AAA58705.1;
                                                                                                                                                                                                                                                                                entities requires a license agreement (some send an email to license@isb-sib.ch).
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                                                                                                                              PIR; 149054; 149054.
MGD; MGI:101901; Klra7.
InterPro; IPR001304; Lectin_C.
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                 DOMAIN
                             Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Ly-49G.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3; Name=Ly-49G.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Ly-49G.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR ON NATURAL KILLER SUBUNIT: Homodimer; disulfide-linked
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   CYTOPLASMIC (: SIGNAL-ANCHOR
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of the Ly-49 gr
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   (POTENTIAL)
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CARBOHYD
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Q8-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NKG2-E type II integral membrane protein (NKG2-E
receptor) (NK cell receptor E).
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This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                      MEDLINE=21623889; PubMed=1179
Shum B.P., Flodin L.R., Muix
Cleland S., Guethlein L.A., U
                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A., ANJ VALLE SEQUENCE FROM N.A., ANJ VALLE SEQUENCE FROM N.A., D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S. Cleland S., Guethlein L.A., Uhrberg M., Parham P., "Conservation and variation in human and common chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLRC3 OR NKG2E.
                                                                                                                           IMMUNOI. 168:240-252 (2002).

TOTALOS PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MECCILS IN THE RECOGNITION OF MECCILS AND SOME CYTOTOXIC T-CELLS.

SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.

SUBCELLULAR LOCATION: Type II membrane protein.

TISSUE SPECIFICITY: NATURAL KILLER CELLS.
                                                                                                         SIMILARITY: Contains 1 C-type lectin family
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Wang H., Gao X., Li L., Lou H., Hua
"Human asialoglycoprotein receptor
human neuroblastoma cells.";
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Receptor; Transmembrane; Multigene
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"Sequence of himan asialoglycoprotein rec
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J. Biol. Chem. 260:1979-1982(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P70194;
01-NOV-1997
01-NOV-1997
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00059; lectin_c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN_2;
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takezawa R., Wagatsuma H., Nomoto C., Watanabe Y., Akaike T., Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel.
C-type lectin 13
CLECSF13 OR KCLR.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D88577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE=Liver;
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InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
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                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                              Endocytosis.
                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                            PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBI outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equires a license agreement (S email to license@isb-sib.ch).
                                                                                       Conservative
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                                                                                         AA;
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                                                                               548
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6126
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41,
                                                                                                                                                                                                                                                                                                                            69
                                10.9%;
26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                         MW;
              25;
Score 138; LL
Pred. No. 5.7e-
25; Mismatches
                                                                                   (POTENTIAL).

EXTRACELLULAR (POTENT C-TYPE LECTIN (SHORT BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLONAC.

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SIGNAL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oration update) receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548
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                                                                                                                                                                                                                                                                                                                                                                                   Lectin;
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                                DB 1;
.7e-05;
                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
OR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                    (SHORT FORM)
                                                                                                                                                                                                                                                                                     (POTENTIAL)
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              46;
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                                                                                                                                                                                                                                                                                                                                                                                   Signal-anchor;
                                                                                         CRC64;
                                                Length
              Indels
                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                            (POTENTIAL)
                                                  548;
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              16;
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                                                                                                                                                                                                                                                                                                                            PROTEIN)
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LQDENENRIGILQQLAKRFCQYVVKQSELKGTFKGHKCSPCDINWRYYGDSCYGFFRHNL

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RN [5]

RN [5]

RN [5]

RD SQUENCE FROM N.A.

RC TISSUE=Pancreas;

RC MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; Pringold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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CD69_HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early activation antiger C (GP32/28) (Leu-23) (MLR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994
15-SEP-2003
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01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93340630; PubMed=8340758;
Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz
Esch F., Sanchez-Mateos P., Sanchez-Madrid F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                        "Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Ma
"Structure of the gene coding for the human early lymphocyte
activation acrigen CD69: a C-type lectin receptor evo-utionari
related with the gene families of natural killer cell-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93314711;
Ziegler S.F., Rams
Grabstein K.H., He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human earliest lymphocyte activation antigen AIM/CD69, a new mu of the C-type animal lectin superfamily of signal-transmitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Esch F., Sanchez-Mateos F., Sauchez man---
"Molecular cloning, expression, and chromosomal localization
"Molecular cloning, expression, and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93267093; PubMed-8496594; Hamann J., Flebig'H., Strauss M.; "Expression cloning of the early integral membrane protein with a J. Immunol. 150:4920-4927(1993).
                                                                                                                                                                                                                                           receptors
                                                                                                                                                                                                                                                                                                                     MEDLINE=94298875;
                                                                                                                                                                                                                                                                                                                                 TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors
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                                                                                                                                                                                                                                                                                                                                                                                         II membrane glycoprotein activation antigens.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.,
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(Rel. 42, Last amnotation update)
arion antigen CD69 (Early T-cell at
Leu-23) (MLR-3) (EAL) (BL-AC/P26)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                711; PubMed=8100776;
Ramsdell F., Hjerrild K.A., Armita
., Hennen K.B., Farrah T., Fanslow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           23:1643-1648(1993).
                                                                                                                                                                                                                                                                                                                     PubMed=8026529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
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                                                                                                                                                                                                                                                                                                                                                                                                                       of the
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                                                                                                                                                                                                                                                                                                                                                                                                       activation antigen (
a family of natural
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anslow W.C.,
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-WIGLTDQGTEGIWRWVDGT
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                                                                                                                                                         InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                          GO; GO:0005887; C:integral to plasma membrane; GO; GO:0004888; F:transmembrane receptor activi
                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG_PROSITE; PS5041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                    PDB; 1E87; 24-OCT-00.
PDB; 1E8I; 26-SEP-00.
                                                        DOMAIN
                                                                     DOMAIN
                                                                                                             Phosphorylation;
                                                                                                                          Antigen; B-cell;
                                                                                                                                                                                                                                                          PIR; JH0822; JH0822.
                                                                                          TRANSMEM
                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                              L; L07555; AAB46359.1; -. 222576; CAAB3298.1; -. 222576; CAAB3017.1; -. 230426; CAAB3017.1; JOINED. 230430; CAAB3017.1; JOINED. 230429; CAAB3017.1; JOINED. 230428; CAAB3017.1; JOINED. 230428; CAAB3017.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: CONSTITUTIVE SER/THE PHOSPHORIATION IN BOTH N
THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
SIMILARITY: Contains 1 C-type lectin family domain.
DATABASE: NAME=PROW; NOTE=CD guide CD69 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL STACQUIRED DURING LYMPHOID ACTIVATION.

ACQUIRED DURING LYMPHOID ACTIVATION.

INDUCTION: BY ANTIGENS, MITOGENS OR ACTIVATORS SURFACE OF IND B LYMPHOCYTES. BY INTERACTION P75 IL-2R ON THE SURFACE OF NK CELLS.

PIM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd69.htm".
                                                                                                                                                                                                                 107273;
                                                                                                                                                                                                                                                                      BC007037; AAH07037.1;
                                                                                                                                                                                                                         HGNC:1694; CD69.
                       62
67
68
96
173
   99
   AA
                                                                                                               3D-structure
                                                                                                                          Glycoprotein;
           199
199
199
194
186
                                                                                          610
   22559
   Š
          EXTRACELLULAR (
C-TYPE LECTIN (
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
                                                                                       CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II
                                                                              (POTENTIAL)
                                                                                                                        Transmembrane;
 172E2699D2FB8DFB CRC64;
                                                                                                                                                                                          receptor activity;
              (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                  (POTENTIAL)
                                                        (LONG
                                                                                                                        Lectin; Signal-anchor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SURFACE GLYCOPROTEIN
                                                                                                                                                                                           TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               다.
다.
            (LATTINETOG)
                                                                                       MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTIW
                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration r. outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D T CELLS,
EPIDERMAL
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PGCV_BC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOVIN STANDARD; PRT; 3381 AA. PB1282; O77609; O77610; O77611; O77612; 15-DEC-1998 (Rel. 37, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Versican core protein precursor (Large fibroblast (Chondroitin sulfate proteoglycan core protein 2) hyaduronate-binding protein) (GHAP).
                                                                                                                                                                                                                                                                                                                      MEDLINE=92062692; PubMed=1720020;
Perides G., Biviano F., Bignami A.;
"Interaction of a brain extracellular matrix protein
                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 21-53;
                                                                                                                                                                                                                                                                                               Biochim
                                                                                                                                                                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Versican V2 is a major extracellular bovine brain.";
  - [ -
                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zimmermann D.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmalfeldt M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98288320; PubMed=9624174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS VO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissus=Forebrain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                    SUBCELLULAR LOCATION: ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                   chim. Biophys. Acta 1075:248-258(1991).
FUNCTION: May play a role in intercellular signaling and
connecting cells with the extracellular matrix. May take
                                                     TISSUE SPECIFICITY:
                                                                                                                                                                                                                             SUBUNIT: Interacts with
in the central nervous system, and in a number of mesenchymal epithelial tissues; the major isoform v2 is restricted to the central nervous system.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                                                 Name=V3;
                                                                                                            Name=V2;
                                                                                                                                                                                       Event=Alternative splicing; Named
                                                                                                                                                                                                                                          hyaluronic acid
                                                                                                                                                                                                                                                       the regulation of cell motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 CNK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 SPCDINWRYYGDSCYGFFRHNLIWBESKQYCIDMNAILLKIDNRNIVEYIK----ARTHL
                                                                                         IsoId=P81282-3; Sequence=VSP_003080
                                                                                                                                                IsoId=P81282-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                           Comment=Additional
                                                                 IsoId=P81282-4;
                                                                                                                    IsoId=P81282-2; Sequence=VSP_003078,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --WVGLKKEPGHP-WKWSNGKEFN-NWFNV----TGSDKCVFLKNTEVSSMECEKNLYWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRWYGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Bovine).
Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                                                                                                     273:15758-15764 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dours-Zimmermann
                                                                                                                                                                                                                                                                                                                                                                                           78-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniat
Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%;
                                                  Sequence=VSP_003078, VSP_003081;
Y: Cerebral white matter. V0 and V1 are expressed
                                                                                                                                               Sequence=Displayed;
 Disappears after the cartilage development
                                                                                                                                                                         isoforms seem to exist;
                                                                                                                                                                                                                 Secreted;
                                                                                                                                                                                                                                                                                                                                                                                         226-250;
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                                                                                                                                                                                                                               FBLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 137.5; DB
Pred. No. 2e-05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrat
actyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        м. т.
                                                                                                                                                                                                                               (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                           262-277;
                                                                                                                                                                                                                 extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٧2
                                                                                                                                                                                         isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                               matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Winterhalter K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
minantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
                                                                                                                    VSP_003079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             component of
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                                                                                                                                                                                                                                                       rix. May take part
differentiation. 1
                                                                                                                                                                                                                  matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteoglycan)
(PG-M) (Glial)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 199;
                                                                                                                                                                                                                                                                                                                         with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovoidea;
                                                                                                                                                                                                                                                                                                                       hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                             the mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sars
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PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00010; CTVPE LECTIN 1; 1.

PROSITE; PS00041; CTVPE LECTIN 2; 1.

PROSITE; PS00022; EGF 1; 2.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01241; LINK; 1.

PROSITE; PS01241; LINK; 2.

Glycoprotein; Proteoglycan; Lectin; Ex Signal; Repeat; EGF-like domain; Calci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig-
InterPro; IPR003006; Ig-
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000435; Sushi_SCR_CCP.
InterPro; IPR000435; Sushi_SCR_CCP.
DOMAIN
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DISULFID
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
SMART; S
SMART; S
SMART; S
SMART; S
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See i
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as its content is in no was a supported to the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
PRINTS; PR01265; LINKMODULE.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF060456; AAC24358.1; -.
EMBL; AF060457; AAC24359.1; -.
EMBL; AF060458; AAC24360.1; -.
EMBL; AF060459; AAC24361.1; -.
                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                    CHAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                     Signal; Repeat;
Hyaluronic acid
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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- SIMILARITY: Contains 1 in SIMILARITY: Contains 2 in SIMILARITY: Contains 2 in SIMILARITY: Contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 c
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; T42389;
p; P01132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P700008; EGF; 2.
P700047; ig; 1.
P700059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m; PD000918; Link; 2.; SM00032; CCF; 1.; SM00034; CLECT; 1.; SM00179; BGF CA; 1.; SM00179; BGF CA; 1.; SM00445; LINK; 2.
       1337
3074
3112
3161
3280
3280
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173
                                                                                                                                                                                                                                                                                                                                                                        acid; Alternative
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                                                                     3074
3110
3148
3275
3338
131
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3381
147
245
347
                                                                                                                                                                                                                                                                                                                                                                                           an; Lectin; Extracellular matrix; domain; Calcium; Immunoglobulin :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin-like V-type domain.
link domains.
EGF-like domains.
C-type lectin family domain.
Sushi (SCR) domain.
THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
  EGF-LIKE 1.
EGF-LIKE 2. CAI
C-TYPE LECTIN.
SUSHI.
SUSHI.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                  splicing.
POTENTIAL
                                                                                                                                                                                                                                    LINK 2.
GAG-ALPHA
                                                                                                                                                                                      (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN) GAG-BETA.
                                                                                                                                                                                                                                                                                                       VERSICAN CORE PROTEINIG-LIKE V-TYPE.
    SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                           CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sushi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 41
PGCV_RAT STANDARD;
ID PGCV_RAT STANDARD;
AC Q9ERB4; 008592; 038564; Q9R1K4;
DT 16-OCT-2001 (Rel. 40, Created)
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Best Local S
Matches 33
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DISULFID
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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use
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                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley; TISSUE=Lung; Blomberg L.A., Chan W.-Y., Clerch L.,
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15-SEP-2003
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   European
by non-
                                                       SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 link domains.
SIMILARITY: Contains 2 EGF-like domains.
SIMILARITY: Contains 1 C-type lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                             hyalluronic acid.
SUBUNIT: Interacts with FBLN1 (E
SUBCELLULAR LOCATION: Secreted;
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                       FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take par the regulation of cell motility, growth and differentiation.
                                                                                                                                                TISSUE SPECIFICITY: 1 but not in glomeruli.
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ROT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation - Bioinformatics Institute. There are no restrictions on its -profit institutions as long as its content is in no way
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sulfate proteoglycan core protein 2)
binding protein) (GHAP) (Fragments).
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DR SMART; SM00034; CLECT; 1.

DR SMART; SM00179; EGF CA; 1.

DR SMART; SM00409; IG; 1.

DR SMART; SM00446; LIKK; 2.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00041; CTYPE_LECTIN 2;

R PROSITE; PS00022; EGF 1; 2.

R PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

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01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Versican core protein precursor (Large fibroblast

(Chondroitin sulfate proteoglycan core protein 2)
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SEQUENCE OF 1-1692 FROM N.A. (ISOFO)
STRAIN-C57BL/6J; TISSUB-Skin;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K.,
Arakawa T., Hara A., Fukunishi Y.,
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                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6, and Swiss Webster; TISSUE=Brain; MEDLINE=95122551; PubMed=7822336; Ito K., Shinomura T., Zako M., Ujita M., Kimata
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                Zako M., Shinomura T., Ujita M., Ito K., Kimata K.; "Expression of PG-M(V3), an alternatively spliced form of PG-M without a chondroitin sulfate attachment in region in mouse and
                                                                                                                                                                                                                                                                                    proteoglycan generated by alternative splicing.";
J. Biol. Chem. 270:958-965(1995).
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                  tissues.
                                                                                                                                                                                                                           STRAIN=C57BL/6
                                                                                                                                                                                                                                               SEQUENCE
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Konno H., Adachi
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MGD; MGI:102889; CSp92 InterPro; IPR000152; B InterPro; IPR000742; B InterPro; IPR001881; E InterPro; IPR006209; E InterPro; IPR007110; I InterPro; IPR003306; I

Asx hydroxyl.
EGF Ca.
EGF Ca.
EGF Tike.
Ig Tike.
Ig Tike.
Ig MHC.

AK014525; P01132; 1E

1EPG

BAB29411.1; Cspg2

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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchla K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schaik K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi N.,
RA Gustincich S., Hill D., Hofmann M., Fume D.A., Kaniya M., Lee N.E.,
RA Gustincich S., Hill D., Hofmann M., Fume D.A., Kaniya M., Lee N.E.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Roofiguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki V...
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or send a
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a cheween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib-entities.com/documents/
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOId=Q62059-4; Sequence=VSP 003087, VSP_003090;
-- TISSUE SPECIFICITY: V2 is found only in brain.
-- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
-- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-- SIMILARITY: Contains 2 link domains.
-- SIMILARITY: Contains 2 EGF-like domains.
-- SIMILARITY: Contains 1 C-type lectin family domain.
-- SIMILARITY: Contains 1 Sushi (SCR) domain.
-- SIMILARITY: SELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10400671;
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SUBUNIT: Interacts with FBLN1.
SUBCELLULAR LOCATION: Secreted;
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sidan. Chem. 274:20444-20449(1999).

FUNCTION: May play a role in intercellular signaling and connecting cells with the extracellular matrix. May take connecting cells with the extracellular matrix. May take
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D28599; -; NOT_ANNOT
D32040; BAA06802.1;
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                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                               ANNOTATED_CDS
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SMART; SM00032; CCP; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00179; EGF CA; 1.

SMART; SM00409; IG; 1.

SMART; SM004045; LINK; 2.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00015; C_TYPE_LECTIN_1; PROSITE; PS00041; C_TYPE_LECTIN_2; PROSITE; PS00022; EGF 1; 2.

PROSITE; PS001186; EGF 2; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01835; IG_LIKE; 1.

PROSITE; PS01835; IG_LIKE; 1.
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PF00084; sushi; 1.
PF00193; Xlink; 2.
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TISSUB-Lung fibroblast;
MEDLINE-88007514; PubMed=2820964;
Krusius T., Gehlsen K.R., Ruoslahti E
"A fibroblast chondroitin sulfate pro
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T Biol. Chem. 262:13120-13125(1987).
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P13611; P20754; Q13010; Q13189; Q15123; Q9UNW5;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial
                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=90059882; PubMed=2583089;
MEDLINE=90059882; PubMed=2583089;
Zimmermann D.R., Ruoslahti E.;
"Multiple domains of the large fibroblast proteoglycan, versican.";
EMBO J. 8:2975-2981(1989).
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MEDILINE=95105108; PubMed=7528742;
Maso M.F., Zimmermann D.R., Iozzo R.V.;
"Characterization of the complete genomic structure of the versican gene and functional analysis of its promoter.";
J. Biol. Chem. 269:32999-33008(1994).
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SEQUENCE OF 2711-3396 FROM N.A.
TISSUE=Lung fibroblast;
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TISSUE-Glial tumor;
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A -> G (IN REF. 3).
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MW; 071B80026BC0762D CRC64;
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MEDLINE=93122792; PubMed=1478664;
Nozo R.V., Nasc M.F., Cannizzaro L.A., 1
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"Differential expression of versican isoforms
J. Neuropathol. Exp. Neurol. 55:528-533(1996)
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"Expression of PG-M(V3), an alternatively
without a chondroitin sulfate attachment :
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Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuropathol. E:
- FUNCTION: May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol.
                                              DEVELOPMENTAL STAGE: Disappears after the cartilage development. SIMILARITY: Contains 1 immunoglobulin-like V-typs domain. SIMILARITY: Contains 2 link domains. SIMILARITY: Contains 2 EGF-like domains. SIMILARITY: Contains 1 C-type lectin family domain. SIMILARITY: Contains 1 C-type lectin family domain. SIMILARITY: Contains 1 SIMILARITY: Contains 1 SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hyaluronic acid.
SUBUNIT: Interac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reducipation. EXP. Neurol. 55:528-533(1996).
FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part tonnecting cells with the extracellular matrix. May take part to regulation of cell motility, growth and differentiation.
                                                                                                                                                           neurofibromas, and and gliomas; v3 is medulloblastomas.
                                                                                                                                                                                                                              TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                              Name=Vint;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLUL
                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named Comment=Additional isoforms seen
                                                                                                                                                                                                             ij
                 SWISS-PROT
                                                                                                                                                                                                                                                                                                          IsoId=P13611-3;
                                                                                                                                                                                                                                                                             IsoId=P13611-4;
                                                                                                                                                                                                                                                                                                                                           IsoId=P13611-2;
                                                                                                                                                                                                                                                                                                                                                                          IsoId=P13611-1;
                                                                                                                                                                          IsoId=P13611-5; Sequence=VSP 003086;
SSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed
normal brain, gliomas, medulloblastomas, schwannomas,
urofibromas, and menningiomas; v2 is restricted to normal brain
d gliomas; v3 is found in all these tissues except
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY
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 the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interacts with FBLN1 (By similarity)
LAR LOCATION: Secreted; extracellular
 Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270:3914-3918(1995).
               entry
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                                                                                                                                                                                                                                                                                                     Sequence=VSP_003084;
                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_003082,
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                                                                                                                                                                                                                                                                            Sequence=VSP
                                                                                                                                                                                                                                                                                                                                                                           Sequence=Displayed;
copyright.
tute of Bic
ght. It is produced through a collaboration Bioinformatics and the EMBL outstation -
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SMART; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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SMART; SM00032; CCP; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00109; EGF_CA; 1.

SMART; SM00109; IG; 1.

SMART; SM00449; IG; 1.

SMART; SM00445; LINK; 2.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00041; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00186; SGF_2; 1.

PROSITE; PS01186; SGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.
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EMBL; X15998; CAA34128.1; --
EMBL; S52488; AAB24878.1; --
EMBL; U26555; AAA67565.1; --
EMBL; D32039; BAA66801.1; --
EMBL; J02814; AAA36437.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005204; F:chondroitin sulfate proteoglycan;
GO; GO:0005540; F:chyaluronic acid binding activity;
GO; GO:0008037; P:cell recognition; TAS.
GO; GO:0007275; P:development; TAS.
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HSSP; P01132; 1EGF.
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InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR005209; EGF_Like.
InterPro; IPR007110; Ig-Tike.
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F00193; xlink; 2.
PD000918; Link; 2.
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; IPR000538; Link.
; IPR000538; Sushi_/
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Ig_MHC.
Lectin_C.
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C-TYPE LECTIN.
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GAG-ALPHA
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IG-LIKE V
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RESULT
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Q90953; Q90945;
C1-NCV-1997 (Rel
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CHICK
PGCV_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90953; Q90945; C1-NCV-1997 (Rel. 35, Created)
C1-NCV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast
Versican core protein precursor (Large fibroblast)
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                                                                                                                                                                                                                                                     STRAIN=White leghorn; TISSUE-Limb bud;

MEDLINB=93300846; PubMed=8314802;
Shinomura T., Nishida Y., Ito K., Kimata K.;
Shinomura T., Nishida Y., Ito K., Kimata K.;

"cDNA cloning of PG-W, a large chondroitin sulfate proteoglycan expressed during chondrogenesis in chick limb buds. Alternative spliced multiforms of PG-M and their relationships to versican."

J. Biol. Chem. 268:14461-14469(1993).

-i- FUNCTION: May play a role in intercellular matrix. May take par the regulation of cell motility, growth and differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
    \frac{1}{1} \ \frac{1}{1} \ \frac{1}{1} \ \frac{1}{1}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa;
 (By similarity).
- SIMILARITY: Contains 1 in SIMILARITY: Contains 2 line SIMILARITY: Contains 2 ENMILARITY: Contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 2 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 contains 1 co
                                                                      TISSUE SPECIFICITY: Prechondrogenic oc
developing limb buds.
DEVELOPMENTAL STAGE: Disappears after
                                                                                                                                                                           hyaluronic acid.
SubcELLULAR LOCATION: Secreted; extracellular matrix.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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                                                                                                                                       Name=V1
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                                                                                                                                                     IsoId=Q90953-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRQKSNEVWKWEDGSVIS-ENM-----FEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLM
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Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%;
                                                                                                      Sequence=VSP_003093;
Y: Prechondrogenic co
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1 immunoglobulin-like \
2 link domains.
2 EGF-like domains.
1 C-type lectin family
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N-LINKED (GLCNAC.....
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Pred. No. 0.00
23; Mismatches
 lectin family domain
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differentiation. E
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SMART; SM00034; CLECT; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00409; IG; 1.

SMART; SM00400; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00041; C_TYPE_LECTIN 1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS0012; EGF 1; 2.

PROSITE; PS00187; EGF_CA; 1.

PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

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                                         MEDLINE=93052405; PubMed=1294118; Kim S. J., Ruiz N., Bezouska K., D "Organization of the gene encodin receptor (MRC1).";
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    Feinberg H., Park-Snyder S., Kol
Weis W.I.;
  Genew; HGNC:7:
MIM; 153618;
GO; GO:000588
GO; GO:000553
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macrophage mannose receptor.";
J. Biol. Chem. 275:21539-21548 (2000).
-i- FUNCTION: MEDIATES THE ENDOCYTOSIS
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Taylor M.E., Bezouska K., Drickamer K.;
"Contribution to ligand binding by multiple or domains in the macrophage mannose receptor.";
J. Biol. Chem. 267:1719-1726(1992).
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PDB; 1EGG; 30-AUG-00.
PDB; 1EGI; 30-AUG-00.
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SUBCELLAULAR LOCATION: Type I membrane protein.
MISCELLANEOUS: CRDS 1-3 HAVE AT MOST VERY WEAK AFFINITY FOR CARBOHYDRAUTE. CRD 4 SHOWS THE HIGHEST AFFINITY BINDING AND MULTISPECIFICITY FOR A VARIETY OF MONOSACCHARIDES. AT LEAST (4, 5, AND 7) ARE REQUIRED FOR HIGH AFFINITY BINDING AND ENDOCYTOSIS OF MULTIVALENT GLYCOCONJUGATES.
SIMILARITY: Contains 8 C-type lectin family domains.
SIMILARITY: Contains 1 rigin B-type lectin domain.
DATABASE: NAMS=PROW; NOTE=PROW 2.65-89(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1644341535_g.ht
    GO:0005887;
GO:0005537;
                                                                                                                                                                          M93213; AAA60389,
M93214; AAA60389,
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SMART; SM00458; RICIN; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 6.

PROSITE; PS50041; C_TYPE_LECTIN_2; 8.

PROSITE; PS50023; FIBRONECTIN_2; 1.

PROSITE; PS50231; RICIN B_LECTIN; 1.

Receptor; Signal; Calcium-binding; Transmembrane; Repeat;

Receptor; Signal; Calcium-binding; Transmembrane; Repeat;

Receptor; Signal; Calcium-binding; Transmembrane; Repeat;
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Pfam; PF00652; Ricin B lectin;
PRINTS; PR00013; PNTYPEII
PRINTS; PR00056; ANTIFREBZEII.
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SMART; SM00034; CLECT; 8.
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  AA;
                                166011 MW;
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CYTOPLASMIC (POTENTIAL).

RICIN B-TYPE LECTIN.

RICIN B-TYPE LECTIN.

FIBRONECTIN TYPE-II.

C-TYPE LECTIN 1 (LONG FORM C-TYPE LECTIN 2 (LONG FORM C-TYPE LECTIN 4 (LONG FORM C-TYPE LECTIN 5 (LONG FORM C-TYPE LECTIN 5 (LONG FORM C-TYPE LECTIN 7 (LONG FORM C-TYPE LECTIN 7 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FORM C-TYPE LECTIN 8 (LONG FOR
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EMBL; D16109; BAA03683.1; -.

PIR; A53210; A53210.

HSSP; D07751; ZFW2.

InterPro; IPR000562; FN_Type II.

InterPro; IPR000304; Lectin C.

InterPro; IPR000772; Ricin B. lectin.

Pfam; PF00040; fn2; 1.

Pfam; PF00052; Ricin B. lectin; 1.

PRINTS; PR00013; FNTYPEII.

PRINTS; PR00013; FNTYPEII.
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P49259;
01-FEB-1996
01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
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MEDLINE=94164945; PubMed=7509792;
Ishizaki J., Hanasaki K., Higashino K.-I., Kishino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning of pancreatic group I
J. Biol. Chem. 269:5897-5904(1994)
-i-FUNCTION: MAY HAVE A KEY ROLE IN NORN
OF SECRETORY PHOSPHOLIPASE A2. ALSO E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O., Arita H.;
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NCBI_TaxID=9913;
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-FEB-1996 (Rel. 3
-OCT-2001 (Rel. 4
0 kDa secretory I
                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 8 C-type lectin family domains. SIMILARITY: Contains 1 ricin B-type lectin domain.
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SM00034;
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PD000995; FN Type_II; 1.
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O SNAKE PA2-LIKE
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SMART; SM00458; RICIN; 1.

PROSITE; PS00615; C TYPE LECTIN 1; 3.

PROSITE; PS50041; C TYPE LECTIN 2; 8.

PROSITE; PS50023; FIBRONECTIN 2; 1.

PROSITE; PS50231; RICIN B LECTIN; 1.

Signal; Receptor; Transmembrane; Repeat; Glycoprotein; Lectin.
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                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Low affinity immuncglobulin epsilon FC receptor (Lymphocyte
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MEDLING-94191542; PubMed=8142907; Padlan E.A., Helm B.A.; Phodeling of the lectin-homology don affinity Fc epsilon receptor (Fc eps Receptor 3:325-341(1993).
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NCBI_TaxID=9606;
[1]
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MEDILINE-93038513; PubMed-1417742;
Rose K., Turcatti G., Graber P., Pochon S., Regamey P.-O.,
Jansen K.U., Magnenat E., Aubonney N., Bonnefoy J.-Y.;
"Partial characterization of natural and recombinant human soluble CD23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87118255; PubMed=2949326; Ikuta K., Takami M., Kim C.W., Honjo T., Miyosl Kawabe T., Yodoi J., Yodoi J., Kawabe T., Yodoi J., Foreceptor for IgE: sequence "Human lymphocyte Fc receptor for IgE: sequence cloned cDNA with animal lectins."; Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=87051737;
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Kilchherr E., Frost H., Delespesse (
"Cloning and expression of the cDNA
receptor.";
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Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R.,
Tsunasawa S., Sakiyama F., Suemura M., Kishimoto T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two species of human fc epsilon receptor II tissue-specific and IL-4-specific regulation Cell 55:611-618(1988).
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                                                                                                                                                                 Protein Sci. 5:240-247(1996).
-!- FUNCTION: THIS RECEPTOR HAS
IGE PRODUCTION AND IN THE DI
CELL-SPECIFIC ANTIGEN).
-!- SUBCELLULAR LOCATION: TYPE I
SCLUBLE EXCRETED FORM.
                                                                                                                                                                                                                                                                            Bajorath J., Aruffo A.;
"Structure-based modeling of the ligand binding of
cell surface receptor CD23 and comparison of two
derived molecular models.";
                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE MODELING MEDLINE=96276216; Pub
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IsoId=P06734-2; Sequence=VSP_003057; PTM: N- AND O-GLYCOSYLATED.
MISCELLANEOUS: THERE ARE TWO KINDS OF DIFFER IN BOTH STRUCTURE AND FUNCTION:
                                                                            Name=B;
                                                                                                               Name=A
                                                                                                                              Event=Alternative
                                                                                                                                                 ALTERNATIVE PRODUCTS:
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PubMed=8745401;
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WA coding
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Hardy R.R., Hirano
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     FC RECEPTORS FOR IGE, WHICH : HIGH AFFINITY RECEPTORS ON
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CONFLICT
STRAND
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PROSITE; PSO0615; C TYPE LECTIN 2; 1.

1 25-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell Repeat; Lectin; Signal-anchor; Alternative splicing; 3D-structure.

CHAIN 1 321 MEMBRANE BOUND FORM.

1 321 SOLUBLE FORM.

SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the SWISS INSTITUTE. There are no resultance. The Buropean Bioinformatics Institute. There are no resultance is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is seen to see the statement of the second statement is not removed.
                                                                         STRAND
TURN
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
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EMBL; X04772; CAA28465.1;
EMBL; M23562; AAA52433.1;
PIR; A26067; LNHUER.
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PDB; 1KJE; 03-APR-96.
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AND MONOCYTES.
- SIMILARITY: Contains 1
- DATABASE: NAME=PROW; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 C-type lectin family domain. DATABASE: NAME=PROW; NOTE=CD guide CD23 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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MW;
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78
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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F86708C0E6515B87 CRC64;
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SIMILARITY
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan (245 kba early postnatal core glycoprotein) [Contains: 150 kDa adu
                                                                                                -!- PIM: TWO ISOPORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DEGRADATION. THE LARGE ISOFORM IS PREDMIXANT IN EARLY POSTNATAL BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 2 Link domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
              between the Swiss Institute of Bioinforms the European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                           neuronal adhesion and neurite outgrowth.";
J. Cell Biol. 125:669-680(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Margolis R.U., Grumet M.;
"The neuronal chondroitin sulfate proteoglycan neural cell adhesion molecules Ng-CAM/LI/NILE a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rauch U., Karthikeyan L., Maurel F., Margolis R.U., Margolis R.K.; "Cloning and primary structure of neurocan, a developmentally regulated, aggregating chondroitin sulfate proteoglycan of brain." J. Biol. Chem. 267:19536-19547(1992).
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=92406907; PubMed=1326557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                  and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
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non-profit institutions as long and this statement is not removed.
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Pred. No. 0.00052;
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Bioinformatics and the titute. There are no restrictions titute. There as its content is in the titute as its content is in the titute.
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and N-CAM, and i
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                                                      a collaboration -
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(NG-CAM
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Query Match
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SMART; SM00034; CLECT; 1.

SMART; SM00103; EGF_CA; 1.

SMART; SM00103; EGF_CA; 1.

SMART; SM00445; LINK; 2.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00015; C_TYPE_LECTIN_1; 1.

PROSITE; PS00041; C_TYPE_LECTIN_2; 1.

PROSITE; PS00022; EGF_1; 3.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01835; IG_LIKE; 1.

PROSITE; PS0184; LINK; 2.
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n; PF00059; lectin_c; 1.
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n; PF00084; xlink; 2.
NTS; PR01265; LINKMODULE.
NTS; PR00356; ANTIFREEZEII.
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Similarity
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EGF like.
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EGF_2.
9.8%;
22.1%;
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EGG-LIKE 2, CALCIUM-BII
EGG-LIKE 2, CALCIUM-BII
C-TYPE LECTIN.
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150 kDa ADULT CORE GLYCOPROTEIN.
IG-LIKE V-TYPE.
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at; Lectin; Su
124;
No. 0.
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shi; Signal.
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EMBL; D17291; BAA04124.1; -
EMBL; D16816; BAA04091.1; -
EMBL; L08010; AAA18204.1; -
PIR; S34591; RGHUIB.
HSSP; P05451; 1LIT.
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D1-FE3-1996 (Rel. 33, Created)
D1-FE3-1996 (Rel. 33, Last sequence update)
28-FE3-2003 (Rel. 41, Last annotation update)
Lithostathine 1 beta precursor (Regenerating
                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe Entropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                              Characterization and possible pathophysiological implications."

EUR. J. Biochem. 230:503-510 (1995).

IF CHICKTON: MIGHT ACT AS AN INHIBITION OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION FORM ALL O-LINKED GLYCANS CONSIST OF GAL-GLCUAC-GAL-GALWAC TETRASACCHARLDE CORE AND GET ELONGATED (MICROHETEROGENEITY)

-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                     De Reggi M., Capon C., Gnarlu D., Miller B.; Fournet B.; The glycan moiety of human pancreatic lithostathine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Pancreas;
TISSUE-Pancreas;
MEDLINE-94153997; PubMed-8110835;
Moriizumi S., Watanabe T., Unno M.,
Moriizumi S., Watanabe T., Okanoto J
Miyashita H., Yonekura H., Okanoto J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=93351647; PubMed=8348956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation, structural (gene, human regI beta." Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95331286;
                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Berge-Lefranc U.;
"A gene homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bartoli
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Eutheria;
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Catarrhini; Hominidae;
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interPro; IPROUSSU,

finterPro; IPROUSSU,

ffam; PROUSS; lectin G;

PRINTS; PRO1504; PACECT; 1.

A SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C TYPE LECTIN 1; 1.

DR PROSITE; PS00615; Lectin; Pyrrolidone carbo...

YOUR CLECT SIGNAL Signal; Lectin; Pyrrolidone carbo...

ET SIGNAL 1 2 BY SIMILARITY BETA.

CHAIN 34 164 C-TYPE LECTIN (LONG FORM).

POD_RES 23 23 PYROLIDONE CARBOXYLIC ACID

MOD_RES 27 27 O-LINKED (GALNAC...) (MUCIN BY SIMILARITY.

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V239_FOWPV
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"Sequence analysis of an il.2 kilobase, near-terminal,
of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
J. Gen. Virol. 69:1025-1040(1988).
                                                                                                                                                                                                           "The genom
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                                                                                                                                                       SEQUENCE OF 1-116 FROM N.A. STRAIN=FP-9 / Isolate HP-43 MEDLINE=88229622; PubMed=28
                                                                                                                                                                                                                                     MEDLINE=20193820; PubMed=10729156;
MEDLINE=70193820; PubMed=10729156;
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                                                                                                                                                                                                                                                                                                  Avipoxvirus
NCBI_TaxID=:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Putative C-type lectin protein FPV239 (BamH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:9952; REGIB.
MIM; 167771;
GO; GO:0008283; P:cell proliferation;
InterPro; IPR001304; Lectin_C.
InterPro; IPR001390; Pancreatis_ac.
                                                                                                                                                                                                                            Afonso C.L., Tulman E.R., Lu Z., "The genome of fowlpox virus.";
                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                            Fowlpox virus
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                                                                                                                                                                     Isolate HP-438;
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Pred. No. 0.00034;
6; Mismatches 53
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(BamHI-ORF8).
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Usage
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[7]
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Title:
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Maximum Match 100%

Listing first 100 summaries
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5: sp_invertebrat;
6: sp_mammal:*
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8: sp_organelle:*
9: sp_plage:*
11: sp_vordent:*
12: sp_virus:*
13: sp_virus:*
13: sp_vertebrate
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15: sp_bacteriap:
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Q8NC01
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Q8BRU4
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Q8BZ31
Q96BA7
Q8CBB4
Q8MJH1
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Q9gme8 pan troglod
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Q54871 rattus norv
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Q8hy10 hylobates 1
Q8hy10 hylobates c
Q8hy11 hylobates c
Q8hy11 hylobates s
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P78380 homo sapien
P79391 bos taurus
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Colonna M., Samaridis J., Angman L.;
"Molecular characterization of two novel Cone of which is selectively expressed in hu
Eur. J. Immunol. 30:697-704 (2000).
EMBL; AF124841; AAP36777.1; -
InterPro; IPR001304; Lectin C.
pfam; pr00059; lectin C.
SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
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    Q8NHR6;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Q9P126;
C1-OCT-2000
C1-OCT-2000
   Similar
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Lectin; Receptor.
SEQUENCE 229 AA; 26700 MW: 019800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TYEMBLTel. 15, Created)
01-OCT-2000 (TYEMBLTel. 15, Last seq
01-MAR-2002 (TYEMBLTel. 20, Last ann
C-type lectin_like receptor-2.
                                                    QBNHR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                    NMFEFLEDGKGNWNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP
                                                                                                                                            LTWEESKQYCTDMNATLLKIDNRNIVE
C-type
                                                   PRELIMINARY;
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  lectin-like
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X MEDINE-20135876; PubMed-10671229;

ACCOINTAM M., Samaridis J., Angman L.;

COINTAM M., Samaridis J., Angman L.;

The color of which is selectively expressed in human dendritic cells.";

The proof which is selectively expressed in human dendritic cells.";

Eur. J. Immunol. 30:697-704(2000).

R MG1; AF201457; AAF368311: -.

DR MG1; AF201457; AAF368311: -.

NR MG1; MG1:1913287; Clacc.

NR InterProof IPRO01304; Lectin_C.

DR Ffam; PF00059; lectin_c; 1.

DR FROSITE; PS50041; C_TYPE_LECTIN_2; 1.

DR FROSITE; PS50041; C_TYPE_LECTIN_2; 1.

SAMART; Receptor.

GW Lectin; Receptor.

SQ SEQUENCE 229 AA; 26239 MW; 1EC9377F491CA52B CRC64;
       Best Loc
Matches
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Best Local Sim
Matches 195;
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Submitted (MAY-2002) to the EMBL/(EMBL, BC02954, AAH29554.1; -..
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITS; PS50041; C_TYPE_LECTIN_2
Receptor; Lectin.
SEQUENCE 196 AA; 23140 MW; 4BJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JL99;
01-OCT-2000
01-OCT-2000
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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     al Similarity
147; Conserv
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     Conservative
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                            62.6%;
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85.2%;
     31;
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Last annotation updat
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Score 790; DB 11;
Pred. No. 2.3e-68;
1; Mismatches 48
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Pred. No. 2.6
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                                                   DB 11;
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Suzuki Y., !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075114; BAC11410.1;
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Interpro; IPR001304; Lectin C.
Pfam; PF00059; lectin C.
Pfam; PF00059; Lectin C.
Pfam; PF00059; Lectin C.
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Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Sait
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari
Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasal
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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yPothetical protein.
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                                                                                                              HPTFCENKHYLMCERKAGMTKVDQL
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                                                                                                                                                ASQSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIDVTSPRSRDCVAILNGMI
                                                                                                                                                                              KARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLED--GKGNMNCAYFHNGKM 203
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Pred. No. 6.2e-26;
3; Mismatches 92
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                                                                    MEDIINE=20135876; PubMed=10671229;
Colonna M., Samaridis J., Angman L.;
"Molecular characterization of two novel Cone of which is selectively expressed in hu Eur. J. Immunol. 30:697-704(2000).
EMBL; AP200949; AAP36830.1; ...
InterPro; IPR001304; Lectin C.
Pfam; PR00059; lectin C; 1.
SMART; SM00034; CLBCT; 1.
PROSITE; PS55041; C TYPE LECTIN 2; 1.
Lectin; Receptor
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SEQUENCE.
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"72; AAH39
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Q8IUW7;
01-MAR-2003
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Mammalia; Eutheria;
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Mammalia; Eutheria;
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SEQUENCE 280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updatin-like receptor-1.
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Pred. No. 7.
Score 346.5; DB 4
Pred. No. 2.4e-25;
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Catarrhini;
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dendritic cells.";
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Best Local
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01-MAR-2003
01-MAR-2003
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome & 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRALN=C575L/6J; TISSUE=Spinal cor
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Weakly similar to C-type lectin-like receptor-1.
Mus musculus (Mouse)
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                                                  SKDCKELRRCACERIAG
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                                                                          PTFCENKHYLMCERKAG
                                                                                                                          ARTH----LIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKG--NMNCAYFHNGKMH 204
                                                                                                                                                  YNKSGGHRCSPCPEKWKWYGDKCYQFYKESKNWQSCEYFCLADNATMLKISTQEELDFAM 184
                                                                                                                                                                          KGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWBBSKQYCTDMNATLLKIDNRNIVEYIK
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Pred. No. 3.5e
12; Mismatches
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Best Local :
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01-JUN-2001
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                    MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbu
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the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
60,770 full-length cDNAs.";
Nature 420:563-573(2002)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Weakly similar to C-type lectin-like receptor-1.
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STRAIN=C57BL/6J; TISSUE=Testis;
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Mammalia; Eutheria;
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SEQUENCE 269
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          Staubli F.,
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Rodentia;
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Rodentia;
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31.5%;
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          Suzuki R.,
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Last sequence update)
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Sciurognathi;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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         Quackenbush
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Best Local
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SEQUENCE
      Sobanov Y., Bernreiter A., Derda
Kalthoff F., Hofer E.;
Kalthoff F., Hofer Of lectin-like
"A novel cluster of lectin-like
dendritic and endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 12, Last annotation update)
Dendritic cell-associated C-type lectin-1 (DECTIN-1
like receptor 1) (Beta-glucan receptor isoform A).
DECTIN-1 OR DECTINI OR BGR.
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                                                                                                                                                                                                                 Yokota K., Takashima A., Bergstresser "Identification of a human homologue cC-type lectin-1, dectin-1.";
                                                                                                                                                                                                                    C-type
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21363425; PubMed=11470510;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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SMART; SM00034; CLECT; l.
PROSITE; PS50041; C_TYPE_LECTI
SEQUENCE 275 AA; 31360 MW;
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Hayashizaki Y.;
"Functional annotation of a full-length mouse
Nature 409:685-690(2001).
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InterPro; IPR001304; Lectin_C.
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MGD; MGI:1918433; 4
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0 MW; C9792BA25C8B5CC2
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Pred. No. 8.4e
18; Mismatches
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No. 8.4e-23;
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Best Local 9
                                                                                             UI-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to C-type (Calcium dependent, carbohydrate)
lectin, superfamily member 12.
Mus musculus (Mouse).
                                                                                                                                                                                                 Q8K1L4
Q8K1L4;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                               NCBI
                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; AV312373; CAC43847.1; -.
EMBL; AY026769; AAK20114.2; -.
EMBL; AF400559; AAL11711.1; -.
Genew; HGNC114558; CLECSF12.
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
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TISSUB-Peripheral blood leukocytes;
Willment J.A., Gordon S., Brown G.D
"Characterization of the human beta
alternatively spliced isoforms.";
J. Biol. Chem. 0:0-0(2001).
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SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2;
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Hermanz-Falcon P., Arce I., Roda-Nav
"Cloning of human DECTIN-1, a novel
expressed on dendritic cells.";
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CE 247 AA;
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                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                        Rodentia;
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0; Mismatches
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                                                  Sciurognathi;
                                                                                    Craniata;
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InterPro; IPR001304; Lectin C.
Pfam; PF00059; Lectin C.
SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20347934; PubMed=10779524; Arizzumi K., Shen G.-L., Shikano S., Xu S., Ritter R. III, Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashi "Identification of a novel, dendritic cell-associated molecule, dectin-1, by subtractive cDNA cloning."; Biol. Chem. 275:20157-20167(2000).
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01-OCT-2000 (TrEMBirel 15, Last sequence up
01-OCT-2002 (TrEMBirel 22, Last annotation
Dendrific cell-associated C-type lectin-1.
CLECSF12 OR DECTIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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InterPro; IPRO01304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
PRINTS; PRO0356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SRQUENCE 244 AA; 27542 MW; F50158025FA80C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; NCBI TaxID=10090;
                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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IGI:1861431; Clecsf12.
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-NYLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWR
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Pred. No. 4
                                                                                                                                               Score 288; DB 11;
Pred. No. 9.1e-20;
2; Mismatches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                  CRC64;
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D Q9H1K3

C Q9H1K3;

C Q9H1K3;

OT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-UN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-CCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Putative transmembrane protein dectin-1 (Dendritic cel C-type lectin-1 beta) (DECTIN-1 receptor) (Lectin-1ike (Beta-glucan receptor isoform 3).

CN DECTIN-1 OR DECTINI OR BGR.

CN DECTIN-1 OR DECTINI OR BGR.

CHAPTER (Fuman).
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Best Local :
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Mammalia; Eutheria; Primates; Catarrhini;
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Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Macaca.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Dendritic cell-associated C-type lectin-1.
Macaca mulatta (Rhesus macaque)
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                   NCBI_TaxID=9606;
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30.1%;
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Virus Dramatically Alters Expression
nd Dendritic Cell Markers During Infec
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Pred. No. 1e-19;
                                                                        Craniata; Vertebrata; Euteleostomi;
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Lectin; Receptor; Transmembrane.
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SMART; SM00034; CLECT; 1.
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J. Biol. Chem. 0:0-0(2001).
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Grunebach F., Bri
"Identification"
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Zhang W., Wan T., Chen T., Cao X.;

"Novel human C-type lectin superfamily member CLI
L Submitted (MAR-2000) to the EMBL/GenBank/DDBJ da'

R EMBL; AF247788; AAL95693.1; -

JR InterPro; IPRO01304; Lectin C.

DR Pfam; PF00059; lectin C; 1.

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C-type lectin protein CLL-1.
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Mammalia, Eutheria, Primates,
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Pfam; PF00059; lectin C; 1.
SMART; SW00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEAASQESQRELKEMIETLAKRLDEKSKKOMELNHQYLNLQEALKRMDNFSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSPWWCPAAVALGVLCLGSLMTIIMLGMQLLQVSDLLKQQQANLTLQENILEGQVLAQQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cuniculus (Rabbit).
Metazoa; Chordata; Craniata;
utheria; Lagomorpha; Leporida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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26.4%;
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Pred. No. 1.3e-17;
3; Mismatches 87
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Catarrhini; Hominidae
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Best Local :
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Q9TTK7;
01-MAY-2000
01-DEC-2001
Lectin-like
                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1."
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                      Biochem. J. 355
EMBL; AB018668;
                                                                                                                                                                                                                                                                              MEDLINE=21181560; PubMed=11284714;
Chen M., Narumiya S., Masaki T., Sawamura T.;
"Conserved C-terminal residues within the lectin-li
are essential for oxidized low-density-lipoprocein
are essential for oxidized low-density-lipoprocein
Biochem. J. 355:289-296(2001).
                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                LAQRQAEKSSQESQRELTEMIETLAHKLDEKSKKLMELQQQNINLQKALEKAANFSG---
 RWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNM---
                                                                                                         GPRSLŠTLRWRPAÁLÍLGILĆIĞLLVTVILLIİQLSQVSDILKQQKVKLTHQEDILEGQA
                                                                                                                                   GP--ASSEWWRVMALILLICVGMVVGLVALGI--
                                                                                      VMQRNYLQDENENR---TGTLQQLAKRFCQYVVKQSELK--
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                   -PCPQDWLWHEENCYKFSSGPFSWEXSRENCLSLDAQLLKINSTDDLEFIQQTIAHSSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NALEFIKSOSRSYDYWLGLSPEEDSTRGMRVDNIINSSAWVIRNAPDLNNMYCGYINRLY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIVEYIKARTHLI-RWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGX
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Cetartiodactyla; Suina;
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26.2%;
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Pred. No. 1.7e
99; Mismatches
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ina; Suidae;
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P78380
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12p13.1-12.
 PROSITE; PS50041; C
Lectin; Lipoprotein;
SEQUENCE 273 AA;
                                                     InterPro; IPR002353; Antifreez InterPro; IPR001304; Lectin C. Pfam; PF00059; Lectin C. Pfam; PF00059; ANTIFREEZBII. SMART; SM00034; CLECT; 1.
                                                                                                                                                                        EMBL;
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                                                                                                                                                                                                                                                                                                                             Strausberg
Submitted
                                                                                                                                                         Genew; HGNC:8133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99047525; PubMed=9828121;
7hang X.Y., Miura K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Li X., Bouzyk M.M.,
"Human oxidized low
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Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The human
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Millar D.S.;
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01-MAY-1997
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В
                                                                                                                                                                  mitted (PEB-2002) to the EMBL/Gen:
L; AB010710; BAA224580.1; -.
L; AJ131757; CAB38175.1; -.
L; AF035776; AAC82329.1; -.
L; AF079167; AAC97927.1; -OINED.
L; AF079164; AAC97927.1; JOINED.
L; AF079165; AAC97927.1; JOINED.
L; AF079166; AAC97927.1; JOINED.
L; AF079166; AAC97927.1; JOINED.
L; BC022295; AAH22295.1; -.
                                                                                                                                                                      ; AF079166; ;
; BC022295; ;
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54:191-199(1998).
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(TrBMBLrel. 23, Last annotation
(TrBMBLrel. 25, Last annotation
OXIDIZED LDL receptor (Oxidised
Telephon 1).
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ייי מיייניתים and assignr
 1; Receptor
30959 MW;
                               TYPE_LECTIN_2;
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Primates;
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Catarrhini; Hominidae;
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Kita T., Masaki T.
dized low-density
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n-type oxidized LDL receptor
iller gene complex with a uni
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Homo.
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Best Local :
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Best Loc
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01-MAY-1997 (TEMBLrel. 03, Last s

01-MAR-2003 (TEMBLrel. 23, Last a

Lectin-like oxidized LDL receptor.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Mammalla; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
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InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
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PF00059; lectin c; 1.
S; PR00356; ANTIFREEZEII.
; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                              Similarity
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 K---ARTHLIRWVGLSRQKSNEVWKWEDGSVISENWPEFLEDGKGNM----
                                                  EVIKBAANYSGPCPQDWLWHEENCYQFSSGSFNWEKSQENCISIDAHILKINSTDELEFI
                                                                                                                  ANITHQEDILEGQILAQRRSEKSAQESQKELKEMIETLAHKLDEKSKKLMELHRQNLNLQ
                                                                                                                                                                                                                    NIKTRKPALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENENRT
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                                                                                                                                                                                                                                                                                                                                                            PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                -CSPCDTNWRYYGDSCYGFFRHNLTWESKQYCTDNNATLLKIDNRNIVEYI
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                                                                                                                                                                                                                                                         19.2%; Sc.
25.2%; Pr
Ltive 54;
                                                                                                                                                                                                                                                                                                                            30892 MW;
                                                                                                                                                                                 -GFVSSWRWYPAAVTLGVLCLGLLVTVILL----ILQLSQVSDLIKKQQ
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Pred. No. 5.5e-16;
0; Mismatches 78
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minantia; Pecora;
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the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length CDNAs.";
                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Acrta and
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                         01-MAR-2003 (TYEMBLIFE) 23,
01-MAR-2003 (TYEMBLIFE) 23,
01-MAR-2003 (TYEMBLIFE) 23,
Eypothetical C-type lectin (Mus musculus (Mouse)
                                         The FANTOM Consortium, the RIKEN Genome Explo
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420.563-573(2002).
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                                       Craniata;
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Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001
01-DEC-2001
                                                                               Q96PA7
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Nature 420:563-573(2002).
EMBL; AX036846; BAC2905.1; -
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STRALN=C57BL/6J, TISSUE=Vagina;
STRALN=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Phikarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Phikarvota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TIEMBLIFE). 23, Created)
01-MAR-2003 (TIEMBLIFE). 23, Last sequence update)
01-MAR-2003 (TIEMBLIFE). 23, Last annotation update)
Weakly similar to C-type lectin-like receptor-1.
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EMBL; AK041288; BAC30890.1;
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                                                                                                                                                                                                                                                                                                                                                                                                               1 MQDEDGYITL----NIKTRK--PALVSVGPASSFWWRVMALILLILCVGMVVGLVALGIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                               YNKSGGHGCSPCPEKWKWYGDKCYOFYKESKNWQSCEYFCLADNATMLKISTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                           KGTFKGHKCSPCDTNWRYYGDSCYGFFRENLTWEESKQYCTDMNATLLKIDNR
                                                                                                                                                                                                                                                                             FFQFYQLSNIQQDSITEKDEKLGNMSRQLQSLQAQNRKLIETLQQVAVKLCR
                                                                                                                                                                                                                                                                                                                                                                  LDDDDTTTSLYSGTSTVTRRABÉRHSENGTPSSV-WRPVALTLLTLCLVLLVGLAALGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 AA;
       (TrEMBLrel.
                                                                          FRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Last sequence update)
                          Created)
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Pred. No. 1.
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Pred. No. 1.7e-14;
4; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 24
Q8CBB4
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Best Local S
Matches 64
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Best Local :
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                                                                                                                                                                                                                                                                                                                   Q8CBB4
Q8CBB4;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                       The FANTOM Consortium, the RIXEN Genome Exploration Research "Analysis of the mouse transcriptome be 60,770 full-length cDNAs.", Nature 420:563-573(2002).

EMBL, AKO36399; BAC29411.1; -...
                                                                                                   Hypothetical protes
                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical C-type lectin domain containing protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF400599; AAL11715.1; -
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin C.
Pfam; PF00059; Lectin C: 1.
PRINTS; PR00356; ANTIFREEZELL
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Willment J.A., Gordon S., Brown "Characterization of the human alternatively spliced isoforms. J. Biol. Chem. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                     l Similarity
64; Conser
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MHABETYTSLQWDIPTSEASQKCQSPSKCSGAWCVVTMISCVVCMGLLATSIFLGIKFFQ
                        MQDEDGYITL--NIKTRKPALVSVGPAS-SFWWRVMALILLILCVGMVVGLVALGIWSVM
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                                                   Score 227.5; DB 1
Pred. No. 8.1e-14;
4; Mismatches 112
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Pred. No. 2.1
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                                                                                                    96EABBEFE1AB57DD CRC64;
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based o
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RESULT DRAWHALL TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO REACH TO RE
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Matches 56
Q8MJH0;
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MEDLINE=22072192; PubMed=12077248;
Guethlein L.A., Flodin L.R., Adams E.J.,
"MX Cell Receptors of the Orangutan (Pong
"MX Cell Receptors of the Orangutan Species_for Tracking the Coevolution of i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor;
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Mammalia; Eutheria;
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Natural killer cell lectin-like receptor
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01-OCT-2002
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56; Conservative
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                                                                                                                                                                                                         KS----YHWMGLIHIPTNGSWQWEDGSILSPNLLTIIEMQXG--DCALYASSFKGYIENC
                                                                                                                                                                                                                                                   KARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCA-YFHNGKMHPTFC
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216 AA;
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                  PRELIMINARY;
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(TrEMBLrel. 22, Last sequence up
(TrEMBLrel. 23, Last annotation
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29.3%; Prof
ative 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 222; DB 6;
Pred. No. 1.9e-13;
7; Mismatches 60
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                PRT;
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n of Killer Cell
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Best Local (
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01-MAY-1999 (TremBLrel.
01-MAR-2003 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                054709
054709;
                                                                                                "Murine Nkg2d and Cd94 are clustered within and are expressed independently in natural ; Proc. Natl. Acad. Sci. U.S.A. 95:6320-6325(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKG2-D protein.
NKG2D OR D6H12S2489E.
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InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM0034; CLECT; 1.
PROSITE; PSG0044
SEQUENCE OF 14-232
STRAIN=C57BL/6;
                                                                                                                                                                                                                        MEDLINE=98263354; PubMed=9600963;
Ho E.L., Heusel J.W., Brown M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                   Yokoyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Natural killer cell lectin-like receptor.
POPY-NKG2D.
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EMBL; AF470404; AAM78504.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Mouse)
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                                                                                            Cd94 are clustered within the natural kindependently in natural killer cells.", Sci. U.S.A. 95:6320-6325(1998).
                                     FROM
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01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                     SEQUENCE
                                                                                                              Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_
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Interpro; IPR001304; Lectin_C.
Pfam; PR00059; Lectin_C:
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                        EMBL; AF259063; AAF86971.1; -. InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                  comparison of chimpanzees
Submitted (AUG-2000) to th
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Khakoo S.I., Rajalingam R.,
Muir D.G., Canavez F., Coop.
Parham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Spleen; STRAIN=C57BL/6J; TISSUE=Spleen;
                                                                                                                                                                                                                                 "Rapid evolution of NK cell receptor systems
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MZ37
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AF030313; AAC28245.1;
AF039026; AAD02117.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                           Similarity
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Q9GLF5;
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01-OCT-2000
01-OCT-2000
01-JUN-2001
NKG2-D.
                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
SEQUENCE FROM N.A. MEDLINE=21291702;
                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                       Immunoreceptor NKG2D.
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LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family members and
identification of novel transmembrane-deleted forms of NKG2-A, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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   PubMed=11398969;
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21585 MW; 7D2CB79EC062FF21
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                                                                                                                                 Euteleostomi;
Sus.
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RAT
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Best Local S
Matches 44
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Best Local :
                                                                                                        SMART; SI
PROSITE;
                                                                                                                                                                      MEDLINE=98281903; PubMed=9620592; Berg S.F., Dissen E., Westgaard I.H., Fossum "Molecular characterization of rat NKR-P2, a expressed by NK cells and resting T cells."; Int. Immunol. 10:379-385(1998).

EMBL; AF00951; AAC40092.1; -
                                                                                                                                      InterPro; IPR002353; AntifreezeII
InterPro; IPR001304; Lectin_C.
Pfam; PP00059; lectin_c; 1.
                                                                                               SEQUENCE
                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                              01-AUG-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                            070215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and NKG2D."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenetics 53:243-249(2001).
        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                       ; PR00356; ANTIFREEZEII.
SM00034; CLECT; 1.
E; PS50041; C_TYPE LECTIN 2; 1.
CE 215 AA; 24438 MW; B49C0364613031AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55;
                                                            Similarity
                     CQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jie H.B., Sot
L.L., Kim Y.B.
       CNKEVSVSSREG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSFKGYTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDQDFFK----LVKSYHWWGLVQIPTNRSWQWEDGSILSPNQITMVEMQNG--SCAVY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIVEYIKARTHLIR---WVGLSRQKSNEVWXWEDGSVISENMFEFLEDGKGNNNCAYFHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PASSFWWRVNALILLILCVGWVVGLVALGIWSVWQRNYLQDENENRIGTLQQLAKRFCQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEMHPIFCEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSPFFLARSIAIAMGIRFIVMVM-----IYSGMIINLLFNQ-
                                                                                                                                                                                                                                                                                                                                            3 (TrEMBLrel. 07,
3 (TrEMBLrel. 07,
3 (TrEMBLrel. 23,
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA;
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                   s (Rat).
Da; Chordata;
ia; Rodentia;
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                                                          16.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.3%;
28.9%;
--YCGPCPNDWICHRNNCYQFFNENKAWNQSQASCLSQNSSLLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization
                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                             Score 204.5; 1
Pred. No. 9.4e.
29; Mismatches
                                                                                                                                                                                                                                                                                                                                          Last sequence up
                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 205; DB 6;
Pred. No. 8.4e-12;
0; Mismatches 65
                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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                                             ).4e-12;
nes 56;
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                                                                 DB 11;
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                                                                                                                                                                                                   S.;
lectin-like receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                             Incels
                                                                   Lergth 215;
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1.5
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                                           Gaps
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                       140
  136
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RESULT 33
Q8MHY9
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Q8SPQ6
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Best Local S
Matches 58
                                            01-OCT-2002 (TrEMBLrel. 22, L
01-MAR-2003 (TrEMBLrel. 23, L
Natural killer cell receptor
POPY-CD94.
                                                                                                                                                                                                                                                                                                                                                                                                            EML; AY075101, ...

EMBL; AY075101, ...

Interpro; IPR001304; Lecci...

Pfam; PF00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

SMART; SM00034; C_TYPE_LECTIN_2; 1.
Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI TaxID=9600;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cow."
Eur. J. I
                                                                                                                         6AHM8ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21858859; PubMed=11870625; McQueen K.L., Wilhelm B.T., Harden K.D., "Evolution of NK receptors: a single Ly4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Cranial Mammalia; Eutheria; Cetartiodactyla; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel 21, Created)
01-JUN-2002 (TrEMBLrel 21, Last sequence up
01-OCT-2002 (TrEMBLrel 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bur. J. Immunol. 32:810-817(2002).
EMBL; AY075101; AAL82800.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8SPQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                   100 NKQLLTKKTSBCDRLNETLQQIKGLSDLVFTEKKGCYHKKKSSESLPNTGELK-----
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                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                          AFSKMENRWKWIDNGIPSRLHLTIMDHRFGKDECAFLTSTRIETIDCYKTYNCIĆEKR
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                SROKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERK 219
                                                                                                                                                                                                                      DTNWRYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKART-HLIRWVGL
                                                                                                                                                                                                                                                                                                              ŚŚVPWHGIAVTĹGÍĹĆLLLLMTITVĹĠÍKISQYILEKHQQEEALWNLSQKYJVVQNDŃYL
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                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                        -----DENENRIGILOQL-----AKRFCQYVVKQSEL---KGTFKGHKCSPC
                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pongo.
                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                           32383 MW;
                                                                                                                                                                                                                                                                                                                                                                           15.9%;
24.4%;
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8
                                                                          Last annotation
                                                                                    Last sequence update)
                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                      Score 200.5; DB 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Butel
actyla; Ruminantia; Pecora;
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RESULT
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Best Local S
Matches 46
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01-JAN-1998
C1-MAR-2003
                                                                                                                                                 EMBL; AF009133; AAC10220.1; -.
InterPro; IFR006209; EGF like.
InterPro; IFR001304; Lectin_C.
Pfam; P700059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                          SEQUENCE 179 AA; 20791 MW; 11E0
                                                                                                                                                                                                                                                                                             MEDLINE=97439492; PubMed=9295048; Dissen E., Berg S.F., Westgaard I.H., "Molecular characterization of a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=F344;
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035778;
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MMBL; AP470380; AAM79480.1; -
EMBL; AP470385; AAM79485.1; -
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
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MEDLINE=22072192;
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                              Similarity
                                                                                                                                                                                                                                                          Immunol. 27:2080-2086(1997)
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n L.A., Flodin L.R., Adams E.J., Parham P.;
Receptors of the Orangutan (Pongo pygmaeus):
for Tracking the Coevolution of Killer Cell Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNALDESCEDKNRYICKQQ
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9 (TrEMBLrel. 23,
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               Conservative
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Pred. No. be 15; Mismatches
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                           Score 196; DB 1
Pred. No. 5e-11;
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                            11E6A55C670EE84C
                                                                                                                                                                                                                                                                                               a gene
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                                              Q8MEY8 PREI
Q8MEY8;
Q1-CCT-2002 (TrE
Q1-CCT-2002 (TrE
Q1-MAR-2003 (TrE
Q1-MAR-1 killer c
POPY-CD94.
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Q8CJC7;
Q1-MAR-2003
01-MAR-2003
01-MAR-2003
        Pongo pygmaeus (Orangutan)
Eukaryota; Metazoa; Chorda
Mammalia; Eutheria; Primat
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6; TISSUE-Spleen; Koike J., Sato H., Shimizu E., Taniguchi M., "Identification and Characterization of a No Submitted (SEP-2000) to the EMBL/GenBank/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF306663; AAN31172.1;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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  TaxID=9600
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                                                                                                                                                                                                                                                                           -EGLH-----HPCPENWVWFRCSCYFFSKEELIWRDSQRACLSLNSSLIRM-NKEEMNFF
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2 (Tremairel. 22, La
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          Chordata;
Primates;
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Rodentia;
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EMBL/GenBank/DDBJ databases.
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9; Mismatches
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Pred. No. 7.
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           Craniata; Vertebrata;
Catarrhini; Hominidae
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Sciurognathi; Muridae;
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           Hominidae;
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                      Euteleostomi;
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MEDLINE=22072192; PubMed=12077248;
Guethlein L.A., Flodin L.R., Adams E.J.,
"NK Cell Receptors of the Orangutan (Pong
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Guethlein L.A., Flodin L.R
"NK Cell Receptors of the
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                                                                                                                                                        NTDELDEMSS-SQQFYWIGLSYSEEHTAWLWENGSSLSQYLFPLFETFNPKNCIAYNPNG
                                                                                                                                                                                                         NRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNG
                                                                                                                                                                                                                                                   EPAPTPGPDIELQKDSDCCSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQ
                                                                                                                                                                                                                                                                                                KQSELKG----TFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWSESKQYCTDMNATLLKID
                                                                                                                                                                                                                                                                                                                                                                                    SSFWWRVMALILLICVGMVVGLVALGIWSVYQRNYLQDENENRTGTLQQLAKRECQYVV
                                                                                                                            KMHPTFCENKHYLMCERK
                                                                                                                                                                                                                                                                                                                                                      TTLWWLISG-TLGIICLSL---MATLGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 AA;
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(TrEMBLrel. 22, Last
(TrEMBLrel. 23, Last
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the Orangutan (Pongo pygmaeus): A Pivotal
he Coevolution of Killer Cell Ig-Like Rec
                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
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                                                                                    177
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Pred. No. 9.8e-1
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Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 179;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
C STRAIN=CB.17 SCID;
CX MIDLINE-98124458; PubMed=9464811;
Vance R.E., Tanamachi D.M., Hanke T., Raulet D.'
RT "Cloning of a mouse homolog of CD94 extends the
"lectins on murine natural killer cells.";
"mmunol. 27:3236-3241(1997).
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Best Local
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01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8K4F1;
Q8K4F1;
01-0CT-2002
01-0CT-2002
01-MAR-2003
                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Naper C., Hayashi S., Lovik G., Kveberg L.,
Dissen E., Ryan J.C., Vaage J.T.;
"Characterization of a Novel Killer Cell Lec
Expressed by Alloreactive Rat NK Cells.";
J. Immunol. 168:5147-5154 (2002).
EMBL; AP416564; AAM22620.1;
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Lectin C.
Fiam. Denonge. loctin C.
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PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
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STRAIN=PV
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                                                                                                                                                                                                                              054708
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Mammalia; Eutheria;
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PROSITE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21990327;
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[1]
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48; Conserv
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Rodentia;
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23.8%;
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Pred. No. 1.5e
36; Mismatches
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                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
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Sciurognathi; Muridae;
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, Murinae; Rat
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Best Local :
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Best Local
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Pfam; PF03054; lectin_N; 1.

PRINTS; PR00356; ANTIFFREZEII.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1

PROSITE; PS50041; C_TYPE_LECTIN_2; 1

Lectin.

SEQUENCE 292 AA; 32337 MW; 54743
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InterPro; IPR006209; EGF like.
InterPro; IPR001304; LecTin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CILECT; 1.
PROSITE; PS50041; C TYPE LECTIN_2; 1.
PROSITE; PS00022; EGF 1; 1.
SEQUENCE 179 AA; 20809 MW; D59E10
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01-NOV-1996 (TrEMBI
01-MAR-2003 (TrEMBI
Macrophage lectin :
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EMBL; D50532; BAA09101.1;
HSSP; P05140; ZAFP.
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                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
InterPro; IPR005640; Lectin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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Q14538;
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Conservative 3
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Primates;
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32; Mismatches
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e binding specif
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InterPro; IPRO01304; Lectin C.
Pfam; PP00059; lectin C; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
SMOO34; CLECT; 1.
SROSITE; PS50041; C_TYPE_LECTIN 2; :
SEQUENCE 223 AA; 24800 MW; B625;
                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003 (TrEMBirel 23, I
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Similar to macrophage lectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat.
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NKR-P1B cDNA.";
xp. Med. 0:0-0(1996)
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                                      FROM N.A.
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(TrEMBLrel.)
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Pred. No. 2e-10;
9; Mismatches
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                                                                                              Craniata; Ve
Catarrhini;
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                                                                                                                    Vertebrata; Eutelecstomi;
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EMBL, AB018004, BAA35123.1;
EMBL, AB018097, BAA35123.1;
EMBL, AB018099, BAA35123.1;
EMBL, AB018099, BAA35123.1;
EMBL, AB018009, BAA35123.1;
EMBL, AB018100, BAA35123.1;
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Piam; PP00059; lectin C; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN
Lectin; Lipoprotein; Receptor.
SEQUENCE 364 AA; 41890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              070156;
070156;
01-AUG-1998
01-AUG-1998
01-CCT-2002
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Nagase M., Hirose S., Fujita T.;
"Unique repetitive sequence and unexpected
"Unique repetitive sequence and unexpected low-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxidized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase M., Abe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99057940; PubMed=9837956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SHR-SP; TIS
MEDLINE=98161826;
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Strausberg R.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC039011;
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              l Similarity
48; Conser
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48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Abe J., Takahashi K., Ando J., Eirose S., Fujir organization and regulation of expression of the low-density lipoprotein receptor (LOX-1) gene.", chem. 273:33702-33707(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLKNAHLVVINSREEQNFVQKYLGSAYTWMGLSDPEG--AWKWVDGTDYATG-FQNWKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQDLKKLTCQVATLNNNASTEGT-----C--CPVNWVEHQDSCYWFSHSGMSWAEAEKYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQQLAKRFCQYVV--KQSELKGTFKGHKCSPCDTNWRYYGDSCYGFFRHNLTWBESKQYC
              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Trembirel. 07, Created)
(Trembirel. 07, Last sequence update)
(Trembirel. 22, Last annotation updat receptor for OXIDIZED LOW-density lip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TISSUE=Kidney;
; TISSUE=Kidney;
:826; PubMed=9494115;
irose S., Fujita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                              i; Receptor.
41890 MW;
                                                                                                                                               TYPE_LECTIN_2;
                               15.1%;
26.1%;
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  Score 190; DB 11;
Pred. No. 4.4e-10;
6; Mismatches 60
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Pred. No. 3.7e-
30; Mismatches
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Sciurognathi;
                                                                                                   0AD2839C07206E09
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LOW-density lipoprotein.
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.7e-10;
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         60;
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                                                   364;
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             Q8K3G1
ID Q8K3G1
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Best Local
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Lectin; Receptor.

285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BDH2;
01-JUN-2001
01-JUN-2001
01-MAR-2002
Killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lymphocytes;
MEDLINE-21361853; PubMed=11369209;
Mager D.L., McQueen K.L., Wee V., Freeman
"Evolution of natural killer receptors: cc
Ly49 and KIR genes in baboon.";
Curr. Biol. 11:626-630(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY028399; AAK26161.1;
HSSP; P05451; 1QDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papio hamadryas (Hamadryas baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLRA-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BDH2
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                                                                                                                       217
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4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
55; Conserv
                                                                                                                                                                                               SCCGVNCYYFIMQKKDWKGCKQTCQHCRSSLLKIDDKDELAFIQSQIYENNYWIGLSYDK
                                                                                                                                                                                                                                                                                     TNKTLKYDILKKDSFLOKKELDSLLMLKSRCHRENEIVLKFLQNTGKFS-
                                                                                                                                                                                                                                                                                                                                                                    WRLIAVTLGILCLFILMIVTVLVTKIFQCVQEKHEQQEILRNCSEKYIMQNDNYLKEQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KANL
                                                                                                              RESKWKWIDNGTSPGINSTIMRSSSGRGECAFLTSTRMATIDCIÇKYNCICEKR
                                                                                                                                                       SNEVWKWEDGSVISENMFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCERK
                                                                                                                                                                                                                                          RYYGDSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKARTHLIR-WVGLSRQK
                                                                                                                                                                                                                                                                                                                                                                                                                 WRVMALILLILCVG--MVVGLVALGIWSVMQRNYLQDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPNHPWLWENGSPLS---FOFFRTRGVSLQMYSSGTCAYIQGGVVFAENCILTAFSICQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KENCY-LFHGPFNWEKSRENCLSLDAQLLQISTTDDLNFV--LQATSHSTSPFWMGLHRK
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           PRELEMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                     --RTGTLQQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33459 MW;
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23.5%;
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17, Last
20, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 189.5; DB 6
Pred. No. 3.7e-10;
1; Mismatches 87
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0C8FDA762B1488FE
                                                                                                                                                                                                                                                                                                                           -LAKRFC----QYVVKQSELKGTFKGHKCSPCDTNW 106
         280
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         ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                     ----EDHW
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Вb
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Best Local S
Matches 54
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01-OCT-2002 (TrEMBLrel. 22, C
01-OCT-2002 (TrEMBLrel. 22, I
01-MAR-2003 (TrEMBLrel. 23, I
Ly49 inhibitory receptor 2.
Ly4912.
                                                                                                                                                                                                                                                                                                                                                                  054707;
01-JUN-1998
01-JUN-1998
01-MAR-2003
Killer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE
  Proc.
                                          STRAIN=C57BL/6J;
Heusel J.W., Ho
"Murine CD94.";
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                       Vance
                                                                                                                                                                                             STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054707
                                                                                                          SEQUENCE
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  KLRD1 OR CD94
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SMART; SM00034; CLECT; 1.
PROSITE; PS5C041; C_TYPE_LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Immunol. 32:2031-
EMBL; AY115572; AAM56042.
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STRAIN=PVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY115572; AAM56042.1; -.
InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22110099;
Naper C., Hayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
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                                                                                                                                                e R.E., Tanam
J. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
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                      Natl. Acad.
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54; Conser
                                                                                                       FROM N.A.
                                                                                                                                                                                                                 FROM N.A
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                                                                                                                                                  Tanamachi D.M., I
                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 23, Last armotation update)
Lectin-like receptor, subfamily D, member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                         (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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                                                               B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32:2031-2036(2002).
AAM56042.1; -
                      SCi.
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S., Joly E., But
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                              Rodentia;
                                                                                                                                                                                                                                                                                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32671 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.9%;
23.9%;
                                                               Brown
                      U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LECTIN_2; 1.
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                      À
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                                                            м.с.,
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Last seg
Last ann
                                                                                                                                                                       Hanke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.56
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 188.5;
Pred. No. 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 natural
                      0:0-0(1998)
                                                                                                                                                                                                                                                                            Sciurognathi;
                                                                                                                                                                                                                                                                                                Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474B3E84A96AE021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Butcher G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seguence update)
annotation updat
                                                                                                                                                                  Ŧ.,
                                                               Matsumoto
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                                                                                                                                                                       Raulet
                                                                                                                                                                                                                                                                                                Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
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Suteleostomi;

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CQ9NZS:
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Best Local S
Matches 43
                                                       TISSUE=Lymphoid;
MEDLINB=21150889; PubMed=11265639;
Vitale M., Falco M., Castriconi R., Parolini
Semenzato G., Biassoni R., Bottino C., Morett
"Identification of NKp80, a novel triggering
human natural killer cells.";
                                                                                                                                                                                                                            mapping
Bur. J.
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=20135860;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lectin-like receptor KLRF1 OR ML/KLRF1.
                                                                                                                                                                                                                                                                                          "Human
                                                                                                                                                                                                                                                                                                                                Roda-Navarro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1997) to the EM EMBL; AF030311; AAC38243.1; ---
EMBL; AF037714; AAC33713.1; ---
EMBL; AF039025; AADD2116.1; ---
MGD; MGI:1196275; Klrd1.
                                                                                                                                                                                                                                                                                                             Fernandez-Ruiz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29NZS2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9NZS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mouse natural
NKG2-D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
Butcher S., Cottage A., Cook G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iectin
  . J. Immunol.
L; AF175206; A
L; AJ305370; C
                                                                                                                                                                                                                      un KLRF1, a novel member of the killer cell l
family: molecular characterization, genomic
ing to the NX gene complex and expression ana
J. Immunol. 30:568-576(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKHYLMCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NF-SQTFFWIGMHYSEKRNAWLWEDGTVPSKDLFPEFSVIRPEHCIVYSPSKSVSAESCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKGTFKGHKCSPCDTNWRYYGDSCYGFFRENLTWEESKQYCTDMNATLLKIDNRNIVEYI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WRLMSVIFGIKCLFLMVTLGVLLINSFTIQNIQSTPSPTTTVEFQEVS
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                                                                                                                                                                                                                                                                                            ン P. .
ス E. .
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. 31:233-242(2001).
AAF37804.1; -.
CAC29425.1; -.
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                                                                                                                                                                                                                                                                                                                              Arce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -BCCVCLDKWVGHQCNCYFISKEEKSWKRSRDFCASQNSSLLQPQSRNELSFM
                                                                                                                                                                                                                                                                                                                          PubMed=10671213;
Arce I., Renedo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15, Created)
15, Last sequence update)
22, Last annotation update)
(Activating coreceptor NKp80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors homologous
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DD343419E93B3465 CRC64;
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                                                                                               Parolini S., Z
                                                                                                                                                                                                                                                                                                                        Montgomery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                        molecule expressed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                           analysis.";
                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                          structure,
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Matches 53
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Best Local S
Matches 54
                                                                                                                                                                                                                                     Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUS=Peripheral blood leukocytes;
Willment J.A., Gordon S., Brown G.D.
"Characterization of the human beta-
alternatively spliced isoforms.";
J. Biol. Chem. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96DR9;
                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
                                                                                                                                                                                                                                                         EMBL; AF400597; AAL11713.1; -.
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       Beta-glucan receptor isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001304; Lectin_C;
Pfam; PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTTE; PS50041; C_TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:13342;
                                                       126
                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
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80
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                                                                                                                                                                                                    Similarity
                                                                                                                                        DEDGYTQLHFDSQSNTRIAVVSEKGSCAASPPWRLIAVILGTLCLVILVIAVVLGTMAIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                       YYGDSCYGFFRHNLTWBBSKQYCTDMNATLLKIDNRNIVEYIKARTH
                                                                                              RSNSGSNTLENGYFLSRNKENHSQPTQSSLE---DSVTPTKAVKTT-
                                                                                                                                                               DEDGYTTLNIKTRKPALVSV-----GPASSFWWRVMALILIELCVGMVVGLVALGIWSVM
                                                     IYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSN--
                                                                                                                         QRN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFTSLKKTWTWVDGSPIDSKIF-FIKGPAKENSCAAIKBSKIFSETCSSVFKWICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRQKSNEVWKWEDGSVISENWFEFLEDGKGNMNCAYFHNGKMHPTFCENKHYLMCE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEWIKYQGKCYWESNEMXSWSDSYVYCLERKSHLLIIHDQLEMAFIQKNLRQLNYVWIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNWRYYGDSCYGFERHNLTWEESXQYCTDMNATLLKIDNRNIVEYIKARTHLIR--WVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVSQGVLLKCQKGSCSNATQYED---TGDLK--VNNGTRRNISNKDLCASRSADQTVLCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVALGIWSVMQR-----NYLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQDEERYMTLNVQSKKRSSAQTSQLTFXDYSVTLHWYKILLGISGTVNGILTLTLISLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODEDGYITLNIKTRKPALVSVG-----PASSFWWRVMALI-----
                                                                                                                                                                                                                                     189
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 AA;
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                   21065 MW;
                                                                                                                                                                                                                                                                                                                                                            Primates;
                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                                                                                                                                                   14.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26562 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.7%;
22.9%;
                                                                                                                   YLQDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWR
                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
                                                                                                                                                                                       Score 185; DB
Pred. No. 6.2e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 185.5; DB
Pred. No. 7e-10;
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                   F7DF9F76EA4B6B59
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                                                                                                                                                                                                                                                                                         -glucan
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                                                                                                                                                                                                  ; DB 4;
6.2e-10;
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                                                    ELISDONH
                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                   CRC64;
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                                                                                              -GVLSSPCPPNWI
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